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Matches 118; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Db 3 MRAPAOIFGFLLLFOGTRCDIQMTQSPSSLSASIGERVSLTCRASQDINSYLMWQOKP 62
 1 MGAPAOILGFLLLFPGRCDIQMTQSPSSLSASIGRVSLTCRASQDIGNLHWLQOEP 60

Qy 63 DGTIKRLIYATSSLSGVPKRFSGSGSDYSLTISLSEDFVAYYCLOYASSPYTFGG 120
 61 DGTIKRLIYATSSLSGVPKRFSGSGSDYSLTISLSEDFVAYYCLOYASSPYTFGG 120

Db 123 GTKLEIKR 130
 121 GTKLEIKR 128

Qy 121 GTKLEIKR 128

RESULT 2
 ID KV5H MOUSE STANDARD; PRT; 117 AA.
 P01641:
 21-JUL-1986 (REL. 01, CREATED)
 21-OCT-1986 (REL. 01, LAST SEQUENCE UPDATE)
 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN PRECURSOR V-V REGION (MOPC 173B).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 RN EUTHERIA; RODENTIA.
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 81064681.
 RA MAX E.E., SEIDMAN J.G., MILLER H., LEDER P.;
 RL CELL 21:793-799(1980).
 DR EMBL; X00880; G197444; -.
 DR PIR; A01924; KVM53B.
 DR HSSP; P01607; 1EGV.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 22
 FT CHAIN 23 117 IG KAPPA CHAIN V-V REGION (MOPC 173B).
 FT DOMAIN 23 45 FRAMEWORK 1.
 FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 57 71 FRAMEWORK 2.
 FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 79 110 FRAMEWORK 3.
 FT DOMAIN 111 >117 COMPLEMENTARITY-DETERMINING 3.
 FT DISULFID 45 110 BY SIMILARITY.
 FT NON_TER 117 117
 SO SEQUENCE 117 AA; 12954 MW; 38F2B08C CRC32;

Query Match
 Best Local Similarity 80.0%; Pred. No. 1.09e-125;
 Matches 92; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

Db 3 MRAPAOIFGFLLLFOGTRCDIQMTQSPSSLSASIGERVSLTCRASQDINSYLMWQOKP 62
 1 MGAPAOILGFLLLFPGRCDIQMTQSPSSLSASIGRVSLTCRASQDIGNLHWLQOEP 60

Qy 63 DGTIKRLIYATSSLSGVPKRFSGSGSDYSLTISLSEDFVAYYCLOYASSPYTFGG 117
 61 DGTIKRLIYATSSLSGVPKRFSGSGSDYSLTISLSEDFVAYYCLOYASSPYTFGG 115

Qy 61 DGTIKRLIYATSSLSGVPKRFSGSGSDYSLTISLSEDFVAYYCLOYASSPYTFGG 115

RESULT 3
 ID KV5H MOUSE STANDARD; PRT; 128 AA.
 P01637:
 21-JUL-1986 (REL. 01, CREATED)
 21-OCT-1986 (REL. 01, LAST SEQUENCE UPDATE)
 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN PRECURSOR V-V REGION (T1).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 RN EUTHERIA; RODENTIA.
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 81052342.
 RA ALTENBURGER W., STEINMETZ M., ZACHAU H.G.;

RL NATURE 287:603-607(1980).
 DR EMBL; V00772; G762979; -.
 DR PIR; A01920; KVM5TL.
 DR HSSP; P01607; 1IIF.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 20
 FT CHAIN 21 128 IG KAPPA CHAIN V-V REGION (T1).
 FT DOMAIN 21 43 FRAMEWORK 1.
 FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 69 FRAMEWORK 2.
 FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 77 108 FRAMEWORK 3.
 FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 118 127 FRAMEWORK 4.
 FT DISULFID 43 108 BY SIMILARITY.
 FT NON_TER 128 128
 SO SEQUENCE 128 AA; 14385 MW; 87009E44 CRC32;

Query Match
 Best Local Similarity 57.0%; Score 581; DB 1; Length 128;
 Matches 81; Conservative 18; Mismatches 29; Indels 0; Gaps 0;

Db 1 MRPAOIFGFLLLFOGTRCDIQMTQSPSSLSASIGERVSLTCRASQDINSYLMWQOKP 60
 1 MGAPAOILGFLLLFPGRCDIQMTQSPSSLSASIGRVSLTCRASQDIGNLHWLQOEP 60

Qy 61 DGTIKRLIYATSSLSGVPKRFSGSGSDYSLTISLSEDFVAYYCLOYASSPYTFGG 120
 61 DGTIKRLIYATSSLSGVPKRFSGSGSDYSLTISLSEDFVAYYCLOYASSPYTFGG 120

Db 121 GTKLEIKR 128
 121 GTKLEIKR 128

Qy 121 GTKLEIKR 128

RESULT 4
 ID KV1M HUMAN STANDARD; PRT; 129 AA.
 P04431:
 13-AUG-1987 (REL. 05, CREATED)
 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN PRECURSOR V-I REGION (WALKER).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 RN EUTHERIA; PRIMATES.
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 85014148.
 RA KLOBECK H.G., COMBRIATO G., ZACHAU H.G.;
 RL NUCLEIC ACIDS RES. 12:6995-7006(1984).
 DR EMBL; X00965; G296684; ALT_TERM.
 DR PIR; A01883; K1HOWK.
 DR HSSP; P01607; 2EGW.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 22
 FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION (WALKER).
 FT DOMAIN 23 45 FRAMEWORK 1.
 FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 57 71 FRAMEWORK 2.
 FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 79 110 FRAMEWORK 3.
 FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 120 129 FRAMEWORK 4.
 FT DISULFID 45 110 BY SIMILARITY.
 FT NON_TER 129 129
 SO SEQUENCE 129 AA; 14069 MW; 99925172 CRC32;

Query Match
 Best Local Similarity 54.8%; Score 558; DB 1; Length 129;
 Matches 82; Conservative 20; Mismatches 25; Indels 0; Gaps 0;

Db 3 MRPAOIFGFLLLFOGTRCDIQMTQSPSSLSASIGERVSLTCRASQDINSYLMWQOKP 62
 1 MGAPAOILGFLLLFPGRCDIQMTQSPSSLSASIGRVSLTCRASQDIGNLHWLQOEP 60


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QY 1 MGAPAOILGFLLLFPCTRCDIOMTOSPSLSASVGDVYITTRARAGISLWLAQOEP 60
Db 63 GKAPPLIYAASLSQSGVTSRFGSGCTDFTLTISLQPEDSATYTCOQSYTLITFGQ 122
QY 61 DGTIKRLIYATSSLSGSGVPRFSGSRGSDYSLTISLESDEFAVYCYQYASSPTFFGG 120
Db 123 GTRLEIK 129
QY 121 GTRLEIK 127

RESULT 5
ID KVAL_HUMAN STANDARD: PRT: 117 AA.
AC P01601;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE 01-MAY-1991 (REL. 18, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-I REGION (HK101) (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
[1]
SEQUENCE FROM N.A.
RA MEDLINE: 81098966.
RA BENTLEY D.L., RABBITTS T.H.;
RA NATURE 288:730-733(1980).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 83129397.
RX BENTLEY D.L., RABBITTS T.H.;
RX CELL 32:181-189(1983).
RL EMBL: J00244; G185970; -
DR EMBL: K01322; G185994; -
DR EMBL: K01324; G185998; -
DR EMBL: Y00558; G33177; -
DR PIR: A01881; K1H011.
DR PIR: A21056; A21056.
DR HSSP: P01607; 1DFB.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 22
FT CHAIN 23 >117 IG KAPPA CHAIN V-I REGION (HK101).
FT DOMAIN 23 45 FRAMEWORK 1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 57 71 FRAMEWORK 2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 79 110 FRAMEWORK 3.
FT DOMAIN 111 >117 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 45 110 BY SIMILARITY.
FT NON_TER 117
FT SEQUENCE 117 AA: 12799 MW; B02D3EA1 CRC32;

Query Match
Best Local Similarity 53.48; Score 544; DB 1; Length 117;
Matches 77; Conservative 17; Mismatches 21; Indels 0; Gaps 0;

Db 3 MRVPAOLIGLLILCFPGARCDIOMTOSPSLSASVGDVYITTRARAGISLWLAQOEP 62
QY 1 MGAPAOILGFLLLFPCTRCDIOMTOSPSLSASVGDVYITTRARAGISLWLAQOEP 60
Db 63 GKAPPLIYAASLSQSGVTSRFGSGCTDFTLTISLQPEDSATYTCOQSYTLITFGQ 117
QY 61 DGTIKRLIYATSSLSGSGVPRFSGSRGSDYSLTISLESDEFAVYCYQYASSPTFFGG 115

RESULT 6
ID KVAL_HUMAN STANDARD: PRT: 129 AA.
AC P04432;
DT 13-AUG-1987 (REL. 05, CREATED)
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN PRECURSOR V-I REGION (DAUDI).
DE HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

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OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 85014148.
RA KLOBECK H.G., COMBIATO G., ZACHAU H.G.;
RL NUCLEIC ACIDS RES 12:6995-7006(1984).
DR EMBL: K02134; G185822; -
DR EMBL: X00966; G296685; ALT_TERM.
DR PIR: A01884; K1H0D1.
DR HSSP: P01607; 1FGV.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 22
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION (DAUDI).
FT DOMAIN 23 45 FRAMEWORK 1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 57 71 FRAMEWORK 2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 79 110 FRAMEWORK 3.
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 120 129 FRAMEWORK 4.
FT DISULFID 45 110 BY SIMILARITY.
FT NON_TER 129
FT SEQUENCE 129 AA: 14235 MW; 05B40B5E CRC32;

Query Match
Best Local Similarity 52.98; Score 539; DB 1; Length 129;
Matches 75; Conservative 24; Mismatches 28; Indels 0; Gaps 0;

Db 3 MRVPAOLIGLLILMLRRVRCDIOMTOSPSLSASVGDVYITTRAGHNTNFTSWQOKP 62
QY 1 MGAPAOILGFLLLFPCTRCDIOMTOSPSLSASVGDVYITTRAGHNTNFTSWQOKP 60
Db 63 GKAPPLIYAASLSQSGVTSRFGSGCTDFTLTISLQPEDSATYTCOQSYTLITFGQ 122
QY 61 DGTIKRLIYATSSLSGSGVPRFSGSRGSDYSLTISLESDEFAVYCYQYASSPTFFGG 120
Db 123 GTRVNDK 129
QY 121 GTRLEIK 127

RESULT 7
ID KVAL_MOUSE STANDARD: PRT: 108 AA.
AC P01643;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
DE IG KAPPA CHAIN V-V REGION (MOPC 173).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RX MEDLINE: 76091934.
RA SCHIFF C., FOUGEREAD M.;
RL EUR. J. BIOCHEM. 59:525-537(1975).
CC -I- THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR: A01926; KVM573.
DR HSSP: P01607; 1FAI.
KW IMMUNOGLOBULIN V REGION.
FT SIGNAL 1 23
FT CHAIN 24 108 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 71 FRAMEWORK 3.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 79 108 FRAMEWORK 4.
FT DISULFID 98 108 BY SIMILARITY.
FT NON_TER 108
FT SEQUENCE 108 AA: 11819 MW; EA186054 CRC32;

Query Match
Best Local Similarity 52.78; Score 537; DB 1; Length 108;
Matches 69; Conservative 24; Mismatches 28; Indels 0; Gaps 0;

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Matches 15; Conservative 16; Mismatches 17; Indels 0; Gaps 0

Db 1 DIOMTOTTSSLSASLGRVITSCGASODISGNLYBMVOOKPDGPVKLLIYTTSSLHSGVPS 60
|||||.....:||||||:|||||:|||||:|||||:|||||:|||||
Oy 21 DIOMTQSPSSLSASLGVRVSLTCASODIGINLMWLOQDPGGITKRLIYATSSLSGSGVPK 80
|||||.....:||||||:|||||:|||||:|||||:|||||:|||||

Db 61 RFSGSAGCTDYSLTISBLZPZBIATVYCCOOYSKLPRFGGKTLEIKR 108
|||||.....:||||||:|||||:|||||:|||||:|||||:|||||
Oy 81 RFSGSRGSDYSLTISSEDEFAVYCYCLOYASSPYFPGGTKEIKR 128
|||||.....:||||||:|||||:|||||:|||||:|||||:|||||

RESULT 8 STANDARD; PRT; 108 AA.
ID KYIR_HUMAN AC P01610;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
D DE HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP MEDLINE; 83273707.
RX GONI F., FRANGIONE B.;
RA PROC. NATL. ACADE. SCI. U.S.A. 80:4837-4841(1983).
CC -1- THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY AGAINST
CC 3,4-PYRIDYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC WALDENSTROM'S MACROGLOBULINEMIA.
DR PIR: A01876; KIHWE.
DR HSP: P01607; ZRCW.

KW IMMUNOGLOBULIN V REGION; MONOCLONAL ANTIBODY.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 2 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 3 35 49 FRAMEWORK 2.
FT DOMAIN 4 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 5 57 88 FRAMEWORK 3.
FT DOMAIN 6 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 7 98 107 FRAMEWORK 4.
FT DISULEPID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11840 MM; BBADA251 CRC32;

Query Match 52.6%; Score 536; DB 1; Length 108;
Best Local Similarity 66.7%; Pred.No. 4.48e-99;
Matches 72; Conservative 20; Mismatches 16; Indels 0; Gaps 0

D 1 DIOMTQSPSSLSASGVGDVYTTCRASOGIRINDIMYOORPGTAPAKRLIYGATSSLOSQVPS 60
|||||.....:||||||:|||||:|||||:|||||:|||||:|||||
Oy 21 DIOMTQSPSSLSASLGRVSLTCASODIGINLMWLOQDPGGITKRLIYATSSLSGSGVPK 80
|||||.....:||||||:|||||:|||||:|||||:|||||:|||||

Db 61 RFSGSAGCTEFTLTINSLOPEDPATYYCLOYSPFWFGGCKVEVKR 108
|||||.....:||||||:|||||:|||||:|||||:|||||:|||||
Oy 81 RFSGSRGSDYSLTISSEDEFAVYCYCLOYASSPYFPGGTKEIKR 128
|||||.....:||||||:|||||:|||||:|||||:|||||:|||||

RESULT 9 STANDARD; PRT; 117 AA.
ID KYJ_HUMAN AC P01602;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
D DE IG KAPPA CHAIN PRECURSOR V-I REGION (HK102) (FRAGMENT).
OC HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 81098966.
RA BENTLEY D.L.; RABBITTS T.H.;
RA NATURE 288:730-733(1980).
FL EMBL; J00245; G185982; -.
DR EMBL; Z00001; G33196; -.
DR

DR	PIR: A01882; K1H012.
DR	HSSP; P01607; 1DFB.
KM	IMMUNOGLOBULIN V REGION; SIGNAL.
FT	SIGNAL.
FT	CHAIN
FT	DOMAIN
FT	DOMAIN
FT	DOMAIN
FT	DOMAIN
FT	DOMAIN
FT	DOMAIN
FT	DISULFID
FT	NON_TER
FT	SEQUENCE
SO	SEQUENCE
Query Match	Best Local Similarity
Matches	72; Conservative
Score 531; DB 1; Length 117;	Pred. No. 7.30e-98;
21; Mismatches 20; Indels 0; Gaps 0;	
1	22
23	>117
23	45
46	56
57	71
72	78
79	110
>117	
45	110
117	117
117 AA;	12768 MW; 502CAD00 CRC32;
52.1%;	Score 531; DB 1; Length 117;
63.7%;	Pred. No. 7.30e-98;
21; Mismatches 20; Indels 0; Gaps 0;	
3	MRVPAQLIGLLMLTPAKDCIQMTQSPSTLSASVGDVHTITCRASQISSTLAWYQOKP 62
1	MGADPAQIGIFLLFPGRNCDIQMTQSPSSLSASLGQVSLTCRASODIGINLHWQOEP 60
63	GKARLLIYDASSLSGVSVPKRFSGSGGTFTLISISQDDPATRYCCOQYNS 115
61	DGTRKRLIYATSSLSGVPKRFSGSRGSDYSLTISLSSEDFVAYYCLOQYAS 113
RESULT	10
ID	KV3H_HUMAN
AC	P04207;
DT	20-MAR-1987 (REL. 04, CREATED)
DT	01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT	01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE	IG KAPPA CHAIN PRECURSOR V-II REGION (CLL) (RHEUMATOID FACTOR).
OS	HOMO SAPIENS (HUMAN).
OC	EUKARYOTA; METAEOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA.
OC	EUETHERIA; PRIMATES.
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MELINE; 86177570.
RA	JIRIK F.R., SORSE J., FONG S., HEITZMANN J.G., CURD J.G., CHEN P.P.,
RA	GOLDFETEN R., CARSON D.A.;
RL	PROC. NATL. ACAD. SCI. U.S.A. 83:2195-2199(1986).
DR	EMBL; M12740; G553486; -.
DR	PIR; A01898; K3HUC.
DR	HSSP; P01607; 1AAG.
KM	IMMUNOGLOBULIN V REGION; SIGNAL.
FT	SIGNAL
FT	CHAIN
FT	DOMAIN
FT	DOMAIN
FT	DOMAIN
FT	DOMAIN
FT	DOMAIN
FT	DOMAIN
FT	DISULFID
FT	NON_TER
FT	SEQUENCE
SO	SEQUENCE
Query Match	Best Local Similarity
Matches	73; Conservative
Score 525; DB 1; Length 129;	Pred. No. 2.07e-96;
26; Mismatches 28; Indels 3; Gaps 3;	
1	MEAPQQL-FLILMLPDTTGEIYVNTQSPALSYSPGERATLSRAQSQSNNTLAWYQOK 59
1	MCAPQOIGIFLLFPGRNCDIQMTQSPSSLSASLGQVSLTCRASODIGINLHWQOEP 59
60	PGQPRLLIYGASTATGIPARFSGSGGTFTLISLSQSEDAVYVYCCOQYNNMPMTE 119
60	PQGTIKRLIYATSSLSGVPKRFSGSRGSDYSLTISLSSEDFVAYYCLOQYAS-SPTTF 118

FT	DOMAIN	77	108	FRAMEWORK 3.	COMPLEMENTARITY-DETERMINING 3.
FT	DOMAIN	109	>115		
FT	DISULFID	43	108		BY SIMILARITY.
FT	NON_TER	115	115		
SEQ	SEQUENCE	115 AA:	12986 MW:	9586894F CRC32:	
Query Match					
Best Local Similarity		51.3%:	Score 523:	DB 1:	Length 115:
Matches		74:	Conservative	13:	Mismatches 28: Indels 0: Gaps 0:
Db	1 MRPAQFLGILLMFPEIKCDIKMTQSPSSMTASGERTYITCKASQDINSTLSNFOCKP	60			
Qy	1 MGAPQALIGLELLFPETCRDIQMTQSPSSLSASLQQRVSLTCRASQDIGINLMHWLOEP	60			
Db	61 GKSRTILYANRLVDGVPREFSGSSGQDYSLTISLEDEMGICYCQVDEFP	115			
Qy	61 DGIKRLIYATSSLSGSGVPRKFRSGSGDYSLTISLESEDFVAYYCLOVASSP	115			
RESULT 13					
ID	KV3Q.MOUSE	STANDARD:	PRT:	108 AA.	
AC	P01650:				
DT	21-JUL-1986 (REL. 01, CREATED)				
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)				
DE	01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)				
DE	IG KAPPA CHAIN V-V REGION (UPC 61).				
OS	MUS MUSCULUS (MOUSE).				
OC	EUDARVOTA: METAQOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:				
OC	EUTHERIA: RODENTIA.				
RN	[1]				
RP	SEQUENCE.				
RX	MEDLINE: 79195288.				
RA	VRANA M., RUDIKOFF S., POTTER M.;				
RL	J. IMMUNOL. 122:1905-1910(1979).				
CC	-1- THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT BIND				
CC	BETA(2-1)-FRUCTOFURANOSYL MOIETIES (INULIN).				
DR	PIR: A01929: KVM561.				
DR	HSSP: P01607; 1FVD.				
KW	IMMUNOGLOBULIN V REGION.				
FT	DOMAIN	1	23	FRAMEWORK 1.	COMPLEMENTARITY-DETERMINING 1.
FT	DOMAIN	24	34	FRAMEWORK 2.	COMPLEMENTARITY-DETERMINING 2.
FT	DOMAIN	35	49	FRAMEWORK 3.	COMPLEMENTARITY-DETERMINING 3.
FT	DOMAIN	50	56	FRAMEWORK 4.	COMPLEMENTARITY-DETERMINING 4.
FT	DOMAIN	57	88		
FT	DOMAIN	89	97		
FT	DOMAIN	98	108		
FT	DISULFID	23	88		
FT	NON_TER	108	108		
SEQ	SEQUENCE	108 AA:	11809 MW:	A5B3F462 CRC32:	
Query Match					
Best Local Similarity		50.9%:	Score 519:	DB 1:	Length 108:
Matches		71:	Conservative	17:	Mismatches 20: Indels 0: Gaps 0:
Db	1 DYQMOSPSSLSASGDIYMTQCAQSGTSLNLMPOCKGKAPKRLIYGASITLEDGVP	60			
Qy	21 DIQMOSPSSLSASGQVRVSLTCRASQDIGINLMHWLOEPDGIKRLIYATSSLSGSGVP	80			
Db	61 RFSGRYGTFELTISLEDEDMATYFCLOHSHVPTFGGSGTKLEIKR	108			
Qy	81 RFSGRSGSDYSLTISLESEDFVAYYCLOVASSPYIFGGSGTKLEIKR	128			
RESULT 14					
ID	KV3M.HUMAN	STANDARD:	PRT:	129 AA.	
AC	P18136:				
DT	01-NOV-1990 (REL. 16, CREATED)				
DT	01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)				
DE	IG KAPPA CHAIN PRECURSOR V-II REGION (HIC).				
OS	HOMO SAPIENS (HUMAN).				
OC	EUKARYOTA: METAQOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:				
OC	EUTHERIA: PRIMATES.				

[1]
RN SEQUENCE FROM N.A.
RP MEDLINE; 88171307.
RA KIPPS T.J., TOMHAVE E., CHEN P.P., CARSON D.A.;
RC J. EXP. MED. 167:840-852(1988).
CC -1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCTIC
CC LEUKEMIA.
DR PIR: P10021; KAHUT.
DR HSP: P01607; IDFB.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION (HIC).
FT DOMAIN 21 43 FRAMEWORK 1
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 56 70 FRAMEWORK 2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 78 109 FRAMEWORK 3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 119 129 JKI SEGMENT
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129
SQ SEQUENCE 129 AA; 14070 MW; DD00C369 CRC32;

Query Match 50.9%; Score 519; DB 1; Length 129;
Best Local Similarity 56.9%; Pred. No. 5.84e-95;
Matches 74; Conservative 26; Mismatches 27; Indels 3; Gaps 3;

Db 1 METPAQLL-FLILMLPDTGETIVLTQSPGTLISLSPGERATISCRASQSVSSSYLAWYQO 59
1 MGAPAOILGFLILL-FPGTRCDIQMTQSPSSLSASLGQRYSLTCRASQDIGIN-LHMLQO 58
QY 59 EPDGTIKRLIYATSSLSGSGVPRKRSRSGSDYSLTSSLESEDFVAYCLOAYASSPTFF 119
Db 120 GGGTKVEIKR 129
QY 119 GGGTKLEIKR 128

RESULT 15
ID KVST-MOUSE STANDARD; PRT; 108 AA.
AC P01653;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
IG KAPPA CHAIN V-V REGION (W3082).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RX MEDLINE; 82099361.
RA JOHNSON N., SLANKARD J., PAUL L., HOOD L.;
RL J. IMMUNOL. 128:302-307(1982).
CC -1- THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT BIND
CC BETA(2-1)-FRUCTOFURANOSYL MOIETIES (INULIN).
DR PIR: B92811; KVM82.
DR HSP: P01607; IFVD.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 108 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108
SQ SEQUENCE 108 AA; 11850 MW; 6CA5F4A0 CRC32;

Query Match 50.8%; Score 518; DB 1; Length 108;

Best Local Similarity 65.7%; Pred. No. 1.02e-94;
Matches 71; Conservative 16; Mismatches 21; Indels 0; Gaps 0;
Db 1 DVQMIQSSSSLSASIGDIYVMTQASQGTININLWMPQOKPKAPRLIYGASILEDGVP 60
QY 21 DIQMTQSSSSLSASLGQRYSLTCRASQDIGINLHMLQOEPDGTIKRLIYATSSLSGSGVPK 80
Db 61 RFGSRYGTDFLTITSSLEDEDMATYFCLQHTLYLPTFEGGKLEIKR 108
QY 81 RFGSRSRSGSDYSLTSSLESEDFVAYCLOAYASSPTFFGGTKLEIKR 128

Search completed: Thu Apr 15 17:56:44 1999
Job time : 11 secs.


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RN [1]
RP SEQUENCE FROM N.A.
RA RYU C.J., JIN B.R., CHUNG H.K., HONG H.J.;
RL SUBMITTED (AUG-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; 066190; G1778126; -.
PFAM; PF00047; 19.
KW SIGNAL.
FT SIGNAL. 1 22 POTENTIAL.
FT CHAIN 23 >131 MONOCIONML ANTIBODY KAPPA CHAIN VARIABLE
FT NON_TER 131 131 REGION.
SQ SEQUENCE 131 AA; 14126 MW; AF1C5603 CRC32;

Query Match
Best Local Similarity 56.9%; Score 525; DB 4; Length 131;
Matches 74; Conservative 26; Mismatches 27; Indels 3; Gaps 3;

Db 3 MGAPADL-FLLLMLPDATGEIVLTQSPPTLSLSPGERATFCRASQSYSGYLAWYQ 61
1 MGAPADLGLFLL-PPGTCDIOMTQSPSSLASLGQVSLTCRASQDI-GINLHMLQ 58
QY 59 EPGGTRKRLIYATSSLSGVPKRFSGSGSDYSLTISLSEDFVAYYCLQYASSPYTF 118
Db 122 GPGTKVDIKR 131
QY 119 GGGTKLEIKR 128

RESULT 3
ID 035842 PRELIMINARY; PRT; 262 AA.
AC 035842;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DE 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE ANTI-HIV-1 REVERSE TRANSCRIPTASE SINGLE-CHAIN VARIABLE FRAGMENT.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-HYBRIDOMA;
RX MEDLINE; 96211469.
RA SHAHREN, F., DUAN L., ZHU M., BAGASRA O., POKERANTZ R.J.;
RL EMBL; 048716; G2289026; -.
PFAM; PF00047; 19.
KW RNA-DIRECTED DNA POLYMERASE.
SQ SEQUENCE 262 AA; 27842 MW; AF24DBF6 CRC32;

Query Match
Best Local Similarity 50.7%; Score 517; DB 11; Length 262;
Matches 80; Conservative 20; Mismatches 24; Indels 2; Gaps 2;

Db 2 DIIMTQSPATLSTVPGDRAVSLCRASQSIDFLHWYQKSHSPRLIKYASQSI-SGIP 60
1 DIIMTQSPATLSTVPGDRAVSLCRASQSIDFLHWYQKSHSPRLIKYASQSI-SGIP 60
QY 21 DIIMTQSPATLSTVPGDRAVSLCRASQSIDFLHWYQKSHSPRLIKYASQSI-SGIP 60
Db 61 SRFSGSGSDFTLISLQPEDEFAIYCCQSYSTPTFGQGTLEIKRT 111
1 SRFSGSGSDFTLISLQPEDEFAIYCCQSYSTPTFGQGTLEIKRT 111
QY 80 KRFSGSRGSDYSLTISLSEDFVAYYCLQYASSPYTFGGTKLEIKRADAAPTYSTP 139
1 KRFSGSRGSDYSLTISLSEDFVAYYCLQYASSPYTFGGTKLEIKRADAAPTYSTP 139
Db 121 PSSKLG 126
QY 140 PSSKLG 145

RESULT 4
ID 015982 PRELIMINARY; PRT; 116 AA.
AC 015982;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)

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DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE RHEUMATOID FACTOR C6 LIGHT CHAIN (FRAGMENT).
GN V<KAPPA>1.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RA ERMEL R.W., KENNY T.P., CHEN P.P., ROBBINS D.L.;
RL ARTHRITIS RHEUM. (MUNCH.) 36:380-388(1993).
DR EMBL; 556182; G298561; -.
PFAM; PF00047; 19.
FT NON_TER 1 1
FT SEQUENCE 116 AA; 12528 MW; BFFBD90D CRC32;

Query Match
Best Local Similarity 50.0%; Score 510; DB 4; Length 116;
Matches 74; Conservative 19; Mismatches 22; Indels 0; Gaps 0;

Db 1 DIOMTQSPSTLSASGDRVTITCRASQSISSWLAWYQKPKAPKLLIYKSSLSGVP 60
1 DIOMTQSPSTLSASGDRVTITCRASQSISSWLAWYQKPKAPKLLIYKSSLSGVP 60
QY 21 DIOMTQSPSTLSASGDRVTITCRASQSISSWLAWYQKPKAPKLLIYKSSLSGVP 80
1 DIOMTQSPSTLSASGDRVTITCRASQSISSWLAWYQKPKAPKLLIYKSSLSGVP 80
Db 61 RFSGSGSGDEFTLISLQPEDEFAIYCCQSYSTPTFGQGTLEIKRTVAPSV 115
1 RFSGSGSGDEFTLISLQPEDEFAIYCCQSYSTPTFGQGTLEIKRTVAPSV 115
QY 81 RFSGSGSGDYSLTISLSEDFVAYYCLQYASSPYTFGGTKLEIKRADAAPTY 135
1 RFSGSGSGDYSLTISLSEDFVAYYCLQYASSPYTFGGTKLEIKRADAAPTY 135

RESULT 5
ID 014540 PRELIMINARY; PRT; 113 AA.
AC 014540;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DE 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE HRV FAB 027-VL (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-PBL;
RA ITOH K., SUZUKI T.;
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL; AB006849; D1023047; -.
PFAM; PF00047; 19.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12383 MW; FCEB1F02 CRC32;

Query Match
Best Local Similarity 49.9%; Score 508; DB 4; Length 113;
Matches 71; Conservative 20; Mismatches 18; Indels 0; Gaps 0;

Db 3 ELQMTQSPSLPASYVDRTITCRASQTIINSYLNWYQKPKAPKLLIYKSSLSGVP 62
1 ELQMTQSPSLPASYVDRTITCRASQTIINSYLNWYQKPKAPKLLIYKSSLSGVP 62
QY 21 DIOMTQSPSTLSASGDRVTITCRASQSISSWLAWYQKPKAPKLLIYKSSLSGVP 80
1 DIOMTQSPSTLSASGDRVTITCRASQSISSWLAWYQKPKAPKLLIYKSSLSGVP 80
Db 63 RFSGSGSGDEFTLISLQPEDEFAIYCCQSYSTPTFGQGTLEIKRT 111
1 RFSGSGSGDEFTLISLQPEDEFAIYCCQSYSTPTFGQGTLEIKRT 111
QY 81 RFSGSGSGDYSLTISLSEDFVAYYCLQYASSPYTFGGTKLEIKRA 129
1 RFSGSGSGDYSLTISLSEDFVAYYCLQYASSPYTFGGTKLEIKRA 129

RESULT 6
ID 000619 PRELIMINARY; PRT; 134 AA.
AC 000619;
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE REV25-2 (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE: 97076268.
RA DECOURT C., COGNE M., ROCCA A.:
RL CLIN. EXP. IMMUNOL. 106:357-361(1996).
DR EMBL: S63559; G1911733; -.
PFAM: PF00047; 19.
FT NON_TER 1 134
FT NON_TER 134 134
SQ SEQUENCE 134 AA; 14534 MW; 9F908F98 CRC32;

Query Match
Best Local Similarity 49.4%; Score 503; DB 4; Length 134;
Matches 70; Conservative 32; Mismatches 30; Indels 3; Gaps 3;

Db 1 MEMPADL-FLIWLMPDSEELITQSPATLSVSPERATLSRASQSYINLAWYQOK 59
1 MGPAPAILFELL-PPGRCDIOMTOSPSLSLQGRVSLTCRASQDIGINLHWLQOE 59
60 PGQAPRLIYGASIRANGISARFSGSGGTEFTLNTLSQSDGLALYFCQYGDMPPTF 119
60 PGCTIRLIYATISLQSGVPRFSGSGSDYSLTISLESEDFVAYCLOVAS-SPYTF 118

120 GGCTKLEIKRTVAAP 134
119 GGCTKLEIKRADAP 133

QY

RESULT 7
ID 000288; PRELIMINARY; PRT; 244 AA.
AC 000288;
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE SINGLE-CHAIN FV FRAGMENT (FRAGMENT).
GN SCFV.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN (1)
RP SEQUENCE FROM N.A.
RA KONTERMANN R.E., WING M.G., WINTER G.:
RL NAT. BIOTECHNOL. 15:629-631(1997).
DR EMBL: Y13057; E315275; -.
DR PFAM: PF00047; 19.
FT NON_TER 1 244
FT NON_TER 244 244
SQ SEQUENCE 244 AA; 26127 MW; A4CF148B CRC32;

Query Match
Best Local Similarity 48.9%; Score 498; DB 4; Length 244;
Matches 71; Conservative 18; Mismatches 19; Indels 0; Gaps 0;

Db 137 DIOMTOSPSLSASIGDRYITICRASEGIYHMLAWYQOKPKAPKFLIYKASSIAGAPS 196
21 DIOMTOSPSLSASIGDRYSITCRASODIGINLHWLQOEPDGIKRLIYATISLSGSGVPR 80

Db 197 RESGSGSDFTLTISLQDDDFATYCCOQSYNPLTFGGGTRLEIKR 244
81 RESGSGSDYSLTISLESEDFVAYCLOVASPYTFGGGTRLEIKR 128

QY

RESULT 8
ID 014535; PRELIMINARY; PRT; 113 AA.
AC 014535;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE HRV FAB N6-VL (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN (1)
RP SEQUENCE FROM N.A.

RC TISSUE=PBL.
RA ITOH K., SUZUKI T.:
RL SUBMITTED (AUG-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AB006842; D1023041; -.
DR PFAM: PF00047; 19.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12207 MW; A546C704 CRC32;

Query Match
Best Local Similarity 48.2%; Score 491; DB 4; Length 113;
Matches 70; Conservative 20; Mismatches 19; Indels 0; Gaps 0;

Db 3 ELVMTOSPSLSASVDRYITICRASQISSTILNMTQOKPKAPKFLIYKASSIAGAPS 62
21 DIOMTOSPSLSASIGDRYSITCRASQDIGINLHWLQOEPDGIKRLIYATISLSGSGVPR 80

Db 63 RESGSGSDFTLTISLQDDDFATYCCOQSYNPLTFGGGTRLEIKR 111
81 RESGSGSDYSLTISLESEDFVAYCLOVASPYTFGGGTRLEIKR 129

QY

RESULT 9
ID 043690; PRELIMINARY; PRT; 239 AA.
AC 043690;
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE ANTI-MPL SCFV (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN (1)
RP SEQUENCE FROM N.A.
RA GODDARD A., YUAN J., ZHU Z., CARTER P.:
RL SUBMITTED (FEB-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF048775; G2911502; -.
FT NON_TER 1 239
FT NON_TER 239 239
SQ SEQUENCE 239 AA; 25262 MW; 5B9ABFAC CRC32;

Query Match
Best Local Similarity 48.1%; Score 490; DB 4; Length 239;
Matches 70; Conservative 18; Mismatches 19; Indels 0; Gaps 0;

Db 133 DIOMTOSPSLSASIGDRYITICRASEGIYHMLAWYQOKPKAPKFLIYKASSIAGAPS 192
21 DIOMTOSPSLSASIGDRYSITCRASQDIGINLHWLQOEPDGIKRLIYATISLSGSGVPR 80

Db 193 RESGSGSDFTLTISLQDDDFATYCCOQSYNPLTFGGGTRLEIKR 239
81 RESGSGSDYSLTISLESEDFVAYCLOVASPYTFGGGTRLEIKR 127

QY

RESULT 10
ID 043689; PRELIMINARY; PRT; 244 AA.
AC 043689;
DT 01-JUN-1998 (TREMBLREL. 06, CREATED)
DT 01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE ANTI-HER3 SCFV (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN (1)
RP SEQUENCE FROM N.A.
RA GODDARD A., YUAN J., ZHU Z., CARTER P.:
RL SUBMITTED (FEB-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AF048774; G2911500; -.
FT NON_TER 1 244
FT NON_TER 244 244
SQ SEQUENCE 244 AA; 26025 MW; 47670049 CRC32;

Query Match
Best Local Similarity 48.1%; Score 490; DB 4; Length 244;

Db 61 RFTSGSGTDFLTITISNVOSEDLAEYFCOYNSPYTFGGTKLEIKR 108
 QY 81 RFGSGSRGSDYSLTISLSEDFVAYCLOAYASSPYTFGGTKLEIKR 128

RESULT 15
 ID 061251 PRELIMINARY: PRT: 127 AA.
 AC 061251:

DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
 DE ANTIGEN, B-CELL RECEPTOR PRECURSOR.
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C;
 RX MEDLINE: 96134009.
 RA THIRION S., MOTMANS K., HEYLIGEN H., RAUS J., VANDEVYVER C.;
 IMMUNOGENETICS 43:167-168(1996).
 EMBL: L43368; G899073; -.
 PEFAM: PF00047; 19.

KM SIGNAL.
 FT CHAIN 1 19 POTENTIAL.
 FT CHAIN 20 127 ANTIGEN, B-CELL RECEPTOR.
 SQ SEQUENCE 127 AA: 13656 MW; C096D809 CRC32;

Query Match 45.6%; Score 465; DB 11; Length 127;
 Best Local Similarity 54.7%; Pred. No. 8,73e-80;
 Matches 70; Conservative 25; Mismatches 31; Indels 2; Gaps 2;

Db 1 MGWSCIILFLVATATGVHSDIQLTQSPAIMSAPGKAVTMTCSASSVS-YMNTYQKS 58
 QY 1 MGAPAPDILFLGLPPTGCDIOMTQSPSSLSLGRVSLTCRASODIGINLHWLQEP 60
 Db 59 GTSPEKWIYDTSKLSAGVAPARFTGSGSTSYSLTISNMEADATYYCOQWSSNPFTFGG 118
 QY 61 DGTIKRLIATSSLSGSGVPRKFSGRSGSDYSLTISLSEDFVAYCLOAYASSPYTFGG 120
 Db 119 GTKLEIKR 126
 QY 121 GTKLEIKR 128

Search completed: Thu Apr 15 17:57:32 1999
 Job time : 29 secs.

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QY 163 TGGTAAGCAGACACCTGGACAGGGCCCTGGATGATGATTTGGAAATATTTTCTTGGAAAT 222
Db 197 GGTAGACAAACCTTTGCAGGGAGTTTTCAGAGACAGATGACGCTTGACACATGACACATCC 256
QY 223 GGTGATCTACTACATACATCGAGAGTTTAAGGGGCAAGGCTCATTTGACATGACAGACATCC 282
Db 257 ACGAATCACCCATCATNGAGCGTGAGAGAACCTGATGATCTGACAGACAGGCCCATATATTAC 316
QY 283 TCACGACGACCCCTACATGATGACATCCACAGCGCTGACATCTGAAGACTCTGGCGGTCTATTTC 342
Db 317 TGTGCAGAG 326
QY 343 TGTGCAGAG 352

RESULT 7
LOCUS EST98669 Homo sapiens cDNA 5' end similar to immunoglobulin heavy
DEFINITION chain V region (GB:X61012) (HT:3230).
SI 129670
SI 9611768
KEYWORDS EST.
SOURCE human primer-M13 Reverse library-Human Small intestine.
ORGANISM Homo sapiens
 Eukaryotes; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnini; Homo. 1 (bases 1 to 238)
 Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bull,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chiu,M.-W., Clayton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fitchman,J.L., Georgagen,N.S.M., Glodex,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle Jr,P.S., Kelley,J.M., Klinek,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.S.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pellegrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Fertie,A., Fischer,C., Hastings,G.A., He,W.-W., Hu,J.-S., Greene,J.M., Gruber,C., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Li,H., Meisner,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wang,J., Xu,C., Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,R., Rosen,C.A., Hasselthine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
 Initial Assessment of Human Gene Diversity and Expression Patterns Based upon 52 Million Bases of cDNA Sequence unpublished (1995)

TITLE CONTACT: Venter, J.C.
JOURNAL The Institute for Genomic Research
 932 Clopper Rd, Gathersburg, MD 20878
 Tel: 3018699056
 Fax: 3018699423
 Email: tdbinfo@tdb.tigr.org
 For clone availability, additional sequence and expression information related to this EST, please contact the TIGR database (tdbinfo@tdb.tigr.org).
FEATURES Location/Qualifiers
 source 1. 238
 /organism="Homo sapiens"
 <1..>238
 BASE COUNT 46 a 70 c 69 g 52 t 1 others
 ORIGIN
 Query Match 20.6%; Score 95; DB 16; Length 238;
 Best Local Similarity 74.2%; Pred. No. 1,17e-139;
 Matches 144; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
 43 ATGACATGACCTGGAGACATCTTTTNTTGTGTGACGACGACAGATGCCCATCCATCCAG 102

QY	1	ATGGAATCAGCAGTGGGCTCTTTCTCTTCCCTCCCTGTCATTAATCACTACAGGTCCACATCCGAG	60
Db	103	GTTCAGCTGGTGCATCTCGAGCTGAGGTGAAGAACCCCTGGGCGCTCACTGAGAGTCTCC	162
QY	61	GCTATATCAACACATCTGGGGCTGAGCTGTGAGAGTCTGGGGCGCTCACTGAGAGATGCTC	120
Db	163	TGCAGGCTTCTGGTTTACACCTTTACACAGCTACGGTATCAGCTGGGTGGACAGGCCCT	222
QY	121	TGCAGGCTTCTGGGTACACATTCACAGCTTCAATATGCACTGGGTAAAGACAGACACT	180
Db	223	GGACAGAGGCTTGA	236
QY	181	GGACAGAGGCTTGA	194
RESULT	8		
LOCUS	AA377128	265 bp	EST
DEFINITION	ESR9660 Small intestine I Homo sapiens cDNA 5' end similar to		21-APR-1997
ACCESSION	AA377128		
KEYWORDS	g2029456		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryotes: mitochondrial eukaryotes; Metazoa; Chordata;		
AUTHORS	Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;		
	Homo.		
	1 (bases 1 to 265)		
	Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fulcher,R.A.,		
	Bult,C.J., Lee,N.H., Kirkness,E.F., Weissstock,K.G., Gocayne,J.D.,		
	White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C.,		
	Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,		
	Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghegan,N.S.,		
	Glodde,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,		
	Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,		
	Morono-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,		
	Phillips,C.A., Ryder,S.E., Scott,J.L., Saudex,D.M., Shirley,R.,		
	Small,K.V., Springs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,		
	Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,		
	Dinke,D., Feng,D.-F., Ferris,A., Fischer,C., Hastings,G.A.,		
	He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,		
	Kozak,D.L., Kunsch,C., HungJun,J., Li,H., Meissner,P.S., Olsen,R.,		
	Raymond,L., Wei,Y.F., Wang,J., Xu,C., Yu,G.L., Ruben,S.M.,		
	Dallion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,		
	Fraser,C.M. and Venter,J.C.		
TITLE	Initial assessment of human gene diversity and expression patterns		
JOURNAL	based upon 83 million nucleotides of cDNA sequence		
MEDLINE	Nature 377 (6547 Suppl), 3-174 (1995)		
COMMENT	96026280		
	Other ESTs: THC167579		
	Contact: Kerlavage, AR		
	Bioinformatics		
	The Institute for Genomic Research		
	9712 Medical Center Drive, Rockville, MD 20850 USA		
	Tel: 3018699056		
	Fax: 3018699423		
	Email: arterlavet@tigr.org		
	For clone availability, additional sequence and expression		
	information related to this EST, please check the TIGR Human Gene		
	Index (http://www.tigr.org/tdb/hg1.html)		
	Seq primer: M13 Reverse.		
FEATURES	Location/Qualifiers		
SOURCE	1..265		
	/organism="Homo sapiens"		
	/note="Organ: small intestine; Vector: pBluescript SK-;		
	Site.1: ECORI; Site.2: XhoI"		
	/db_xref="ATCC (inhost):181546"		
	/db_xref="taxon:9606"		
	/clone_lib="Small intestine I"		
	/dev_stage="adult"		
	<1..>265		
BASE COUNT	57 a 69 c 79 g 58 t 2 others		
ORIGIN			

/note="Organ: mammary gland; Vector: pT73D-Pac (Pharmacia) with a modified polylinker. Site.1: Not I; Site.2: Eco RI. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTCACATCTGAGAGTGGAGCGCCGGAGATGTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M. Fatima Bonaldo."

/db_xref="taxon:10090"
/clone="1398374"
/clone_lib="Soares mouse mammary gland NbMAG"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"

BASE COUNT 38 a 32 c 25 g 21 t

Query Match 18.7%; Score 86; DB 17; Length 116;
Best Local Similarity 89.1%; Pred. No. 4,46e-121;
Matches 98; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Db 2 AGAAGTTCAGAACAGCCACACTGACAGACAAATCTCCAGACACCTACATGC 61
|||||
Oy 242 AGAAGTTTAAAGGGGAGGCTCATTTGACAGACATCTCCAGACACCTACATGC 301
|||||
Db 62 AACTCAGACGCTGACATCTGAGACACTGGCTATTACTGTGGAAGA 111
| |||||
Oy 302 AGATCAGCAGCCTGACATCTGAGACACTGGCTATTACTGTGGAAGA 351
| |||||

RESULT 11
LOCUS AA987559 336 bp mRNA EST 23-JUL-1998
DEFINITION or83g01.s1 NCI CGAP LUS Homo sapiens cDNA clone IMAGE:1602480 3' similar to gb:IM87789 IG GAMMA-1 CHAIN C REGION (HUMAN);, mRNA sequence.
ACCESSION AA987559
NID 93172923
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 336)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)

JOURNAL COMMENT
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: Christopher Koskaluk, M.D., Ph.D., Michael R. Emmerit-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILNt at: www-bio.lnlnl.gov/bdnp/image/image.html
Insert Length: 801 Std Error: 0.00
Seq primer: -40m3 fwd. ET from Amerisham
High quality sequence stop: 322.
Location/Qualifiers
1..336
/organism="Homo sapiens"
/note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a modified polylinker. 1st strand cDNA was prepared from a neuroendocrine lung carcinoid, and was then primed with a

Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo."

/db_xref="taxon:9606"
/clone="IMAGE:1602480"
/clone_lib="NCI-CGAP LUS"
/tissue_type="carcinoid"
/lab_host="DH10B"

BASE COUNT 82 a 86 c 100 g 68 t

Query Match 18.4%; Score 85; DB 15; Length 336;
Best Local Similarity 63.8%; Pred. No. 5.00e-119;
Matches 197; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

Db 14 ACAGCTCCAGTCACAGCTCCAGATGAGACACTGAGGCGTGAAGAACCGAGG 73
|||||
Oy 43 ACAGGTCTCCACTCCAGGCTTATCTACAGCAGTGTGGGCTGAGCTGGAGCTGGG 102
|||||
Db 74 TCTTCGTAAGGTACACTGCTTGGCTTGGAGGACCTTCGGTGTGACTGCAC 133
| |||||
Oy 103 GCCTCAGTGAAGATGCTCTGCAAGGCTTGTGCTACACATGACGATTACATATGAC 162
|||||
Db 134 TGGGTGCGACAGGCCCCCTGAGACAGCGCTGAGTGGATGGGGAAGATCCCATCGCT 193
|||||
Oy 163 TGGGTAAACAGACACCTGAGACAGGCTGGAATGATTTGAATTTTCTCGGAAT 222
|||||
Db 194 CATTCAGCACTACGACACCGAAGTTTTCAGACAGATACATAACCCGGCAATCT 253
| |||||
Oy 223 GGTGATCTTACTACATGAAAGTTTAAAGGCAAGCCCTCATGCTCAACACATCC 282
|||||
Db 254 ACGGCTCAGTCTACATGGAATGACACCGCTGATTTTGAAGACGCGCATATATAT 313
| |||||
Oy 283 TCCAGACACGCTCAGTACATGAGATGACACACCTGACATCTGAAGACTCTCGTATTTC 342
|||||
Db 314 TGTGCGAGA 322
|||||
Oy 343 TGTGCAGA 351
|||||

RESULT 12
LOCUS T28938 209 bp mRNA EST 06-SEP-1995
DEFINITION EST61186 Homo sapiens cDNA 5' end similar to immunoglobulin mu heavy chain, VDJ regions (GB:M17751) (Ht:3055).
ACCESSION T28938
NID 9611036
KEYWORDS EST.
SOURCE human primer-M13 Reverse library-Human White blood cells.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Reptapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 209)
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fulmer, R.A., Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gockyne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W., Clayton, R.A., Cline, R.T., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., FitzHugh, W.M., Fritchman, J.L., Geoghegan, N.S.M., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, J.R.P.S., Kelley, J.M., Kline, K.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Sauder, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utechtack, T.R., Weidman, J.F., Li, Y., Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.-J., Dinke, D., Feng, P., Ferrite, A., Fischer, C., Hastings, G.A., He, W.-W., Hu, J.-S., Greene, J.M., Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H., Weissner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wang, J., Xu, C., Yu, G.-L., Ruben, S.M., Dillon, P.J., Fennon, K.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.W. and Venter, J.C.

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OY      121 GTRLEIK 127          |||||:]
                                           ]
RESULT 4
ID       R39569 standard; Protein; 246 AA.
AC       R39569.
DT       07-FEB-1994 (first entry)
DE       Sequence of 520C9 sfv protein.
KW       Single chain Fv polypeptide; VH-VL heterodimer; immunoglobulin; Ig;
RW       biosynthetic single polypeptide chain binding site; ss.
OS       Synthetic.
PN       M09316185-A.
PD       19-AUG-1993.
PF       05-FEB-1993; U01055.
PR       06-FEB-1992; US-831967.
PS       (CEU ) Cetus Oncology Corp.
PA       (CREA-) CREATIVE BIOMOLECULES INC.
PI       Houston IL, Huston JS, Oppermann H, Ring DB;
DR       WPI: 93-272889/34.
DS       N-BSDB: Q46084.
New single chain Fv polypeptide binding to C-erbB-2 tumour
antigen - for imaging or treating breast or ovarian cancer etc.
PS       Claim 4: pages 60-61; 87pp: English.
CC       C-erbB-2 refers to a protein antigen expressed on the surface of
CC       tumour cells, such as breast and ovarian tumour cells, which is an
CC       approx. 200,000 mol. wt. acidic glycoprotein having an isoelectric
CC       pt. of about 5.3 (see Q46083, R39568). A single chain Fv (sfv)
CC       is a covalently linked VH-VL heterodimer which is expressed from
CC       a gene fusion including VH- and VL- encoding genes connected by
CC       a peptide-encoding linker. Such linker sequences are set forth in
CC       AA residues 116-135 in R39569, which includes part of the 16 AA
CC       linker sequences in R39572. Using Q46084 for the 520C9 monoclonal
CC       antibody, a single chain polypeptide can be produced having a
CC       binding affinity for a c-erbB-2 related antigen. 'X' in R39569
CC       refers to the location of a stop codon in Q46084.
SO       Sequence   246 AA;

Query Match           69.2%; Score 705; DB 8; Length 246;
Best Local Similarity 89.4%; Pred.No. 7,40e+43;
Matches    101; Conservative     5; Mismatches    7; Indels    0; Gaps    0;

Db      134 dgmqtgspssjsasjagervslltcrasqdglnslwlgqpdtlkrillyatsidsqvpk 193
        |||||||.....:|||||||.....:|||||||.....:|||||||.....:|||||||
OY      21 DIQMOSPSSSSASAGRVSLTCRASODIGINLHMLQOEPPGTIKRLIYATSSLGSEVPK 80
        |||||||.....:|||||||.....:|||||||.....:|||||||.....:|||||||
Db      194 rfsgsrssdytiltssiesedfvvyycylgaifpyrfggtnleikradsa 246
        |||||||.....:|||||||.....:|||||||.....:|||||||.....:|||||||
On      81 RFSGSRSSSDYSLTITSSLESDDFYAYCYLAQVASSPYTFGGCTKLEIKRADAP 133
        |||||||.....:|||||||.....:|||||||.....:|||||||.....:|||||||

RESULT 5
ID       W27121 standard; Protein; 107 AA.
AC       W27121.
DT       04-JAN-1998 (first entry)
DE       Murine antibody light chain variable region consensus.
KW       Monoclonal antibody 11D10; anti-idiotypic antibody; mucin;
RW       human milk fat globule; HMFG; tumour; breast cancer; vaccine.
OS       Mus musculus.
FH       Key
FT       Region
FT       Location/Qualifiers
FT       /label=CDR1
FT       /note="complementarity determining region 1"
FT       50..56
FT       /label=CDR2
FT       /note="complementarity determining region 2"
FT       88..96
FT       /label=CDR3
FT       /note="complementarity determining region 3"

W09722699-AZ.
PD 26-JUN-1997.
PF 19-DEC-1996; U20757.
PR 13-DEC-1996; US-575762.

```

Query Match	Best Local Similarity	Matches 100%	Conservative	Score 702	DB 25	Length 107	0
1	68.9%	93.58%	3	1,25e-42	4	Indels 0	Gaps 0
21	DIQMTGSSSSLSASLGVNSLTCRASODIGINLHWLQDPDGTIKRLITVSSLSGSGVPK	80					
61	ffsgsgsdydylstlsslsesgdfdydyclyqasapyyffgggtklxk	107					
81	RFGSGRSGSDYSLRTSSLESEDFVAVYCYLQYASSPYFFGGGTKLK	127					
RESULT	6						
ID	W02280	standard; Protein; 243 AA.					
AC	W02280						
DT	29-OCT-1996	(first entry)					
DE	520C9 anti-c-erbB-2 two single chain Fv construct.						
KW	520C9; anti-c-erbB-2 monoclonal antibody; single chain Fv; sfv;						
KW	construct; polypeptide linker; C-terminal amino acid sequence;						
KW	in vivo imaging; drug targeting experiment; homodimer;						
OS	Homo sapiens.						
FT	Key	Location/Qualifiers					
FT	peptide	118..133					
FT		/label= linker					
PN	US5534254-A.						
PD	09-JUL-1996.						
PT	06-FEB-1992; 831967						
PR	06-FEB-1992; US-831967.						
PR	07-OCT-1993; US-133804.						
PA	(CHIR) CHIRON CORP.						
PA	(CREA-) CREATIVE BIOMOLECULES INC.						
PI	Houston IL, Huston JS, Oppermann H, Ring DB;						
DR	WPI: 96-333194/33.						
DR	N-PSDB: T36880.						
PT	Compsns. contg. antigen-targeting antibody fragment constructs						
PT	comprising dimer of single-chain Fv fragments						
PS	Example 1; Columns 33-36; 30pp; English.						
CC	Variable heavy (VH) and variable light (VL) genes were cloned from						
CC	a 520C9 hybridoma cDNA library, using probes directed toward the						
CC	antigen constant and joining regions. A two single chain Fv (sfv)						
CC	gene was constructed by connecting the VH and VL genes with a						
CC	ser rich polypeptide linker. The resulting 520C9 two sfv gene,						
CC	which encodes the present sequence, was inserted into an expression						
CC	vector, transformed into E. coli, and protein expression induced by						
CC	the addn. of IPKG to the culture medium.						
CC	A compsn. comprising a carrier and the 2 sfv protein prod. can be						
CC	used for in vivo imaging, and drug targeting experiments. The						
CC	2 sfv protein prod. is a homodimer, in which both fragments target						
CC	the same antigen, therefore giving greater binding avidity and						

PT recombinant host cells with a secreting replicable genetic
PT display package.
PS Example 46; Fig 52; 109pp: English.
CC The sequence is the light chain of clone MIF encoding an scFv frag-
CC ment specific for both hen and turkey egg lysozyme (HEL and TEL).
CC The DNA encoding the chain was amplified from a cDNA library prep.
CC from the spleen of an unimmunised mouse. The corresponding heavy
CC chain was also amplified from an existing construct, pSM1-VHD1.3
CC (Ward et al, 1989). The two fragments were assembled via a linker
CC to prepare an scFv construct which was ligated into the fDCA72
CC vector for expression on the surface of fd bacteriophage. In this
CC way, the VL domain was replaced by a library of VL domains to allow
CC for selection of a broader range of antibody specificities. Several
CC clones were isolated which bound to TEL (the parent antibody D1.3
CC binds exclusively to HEL). The sequences of the light chains of
CC two of these clones, MFI and M21 are given in R21310 and R21311
CC respectively. The D1.3 light chain is given in R21309.
CC See also R21260-307, 309-312, R22450, R22565, R22567-81.
SQ Sequence 108 AA;

Query Match 67.7%; Score 650; DB 4; Length 108;
Best Local Similarity 90.7%; Pred. No. 9,99e-42;
Matches 98; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Db 1 d1eltgppsslsaslgervsltrcraqdigslnwlgdpdgtlkrllyatssidsyvk 60
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 21 DIQMTQSPSSISASLGVRSLTCRASQDIGINLHMQDEPDGTRKRLIYATSSLSGSGVPK 80
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 rfsgsrsgsdysltsslsesedfvdyclygasspwtffgggtklleikra 108
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 81 RFSGRSGSDYSLTSSLSSEDFVAYVYCLOYASSPYTFGGGTKLEIKR 128

RESULT 10
ID W18271 standard; peptide; 109 AA.
AC W18271;
DE 09-JAN-1998 (first entry)
KW PrP 37 light chain variable region.
KW Prion protein; PrP; heavy chain variable region; antibody; scrapie;
KW light chain variable region; PrP-Sc; pathogen; fatal familial insomnia;
KW central nervous system spongiform encephalopathy; human; therapy;
KW transmissible neurodegenerative disease; Creutzfeldt-Jakob Disease;
KW bovine spongiform encephalopathy; feline spongiform encephalopathy;
KW Serstman-Strassler-Scheinker Disease.
OS Mus musculus.
FT Key Location/Qualifiers
FT Region 1..23
FT Region 24..34 "framework region 1"
FT Region 35..49 "complementarity determining region 1"
FT Region 50..56 "framework region 2"
FT Region 57..88 "complementarity determining region 2"
FT Region 89..97 "framework region 3"
FT Region 98..109 "complementarity determining region 3"
FT Region 109..109 "framework region 4"
FT Region 109710505-A1.
PD 20-MAR-1997.
PE 13-SEP-1996; U14840.
PR 14-SEP-1995; US-528104.
PA (REGC) UNIV CALIFORNIA.
PI Burton DR, Prusiner SB, Williamson RA:
DR WPI; 97-202357/18.
PT New antibodies to the scrapie isoform of prion protein - used for
PT detection of infectious prion proteins or for treating disease such
PT as BSE, CJD or scrapie.
PS Example 9; Fig 6; 99pp: English.
CC W18266-W18285 represent portions of the antibodies of the invention. The
CC antibodies of the invention are able to bind the scrapie isoform of prion

CC protein PrP-Sc in situ. Prions are infectious pathogens that cause
CC central nervous system spongiform encephalopathies in humans and animals.
CC The scrapie isoform of the prion protein (PrP-Sc) is necessary for both
CC the transmission and pathogenesis of the transmissible neurodegenerative
CC diseases of animals and humans. The antibodies can be used in a method of
CC the invention for detecting human PrP-Sc in a source. The antibodies
CC specifically bind to prion proteins associated with disease and do not
CC bind to denatured PrP proteins not associated with disease. They can bind
CC to prion proteins of a specific species of mammals. They can also have
CC the ability to neutralise infectious prions. The antibodies can be used
CC for screening for the presence of prions in products such as
CC pharmaceuticals, food or cosmetics. They can also be used for prion
CC neutralisation to purify products, for extraction of prion proteins or
CC for therapy, for diseases such as bovine spongiform encephalopathy,
CC Creutzfeldt-Jakob Disease, fatal familial insomnia or
CC Serstman-Strassler-Scheinker Disease, scrapie or feline spongiform
CC encephalopathies.
SQ Sequence 109 AA;

Query Match 67.5%; Score 688; DB 25; Length 109;
Best Local Similarity 89.0%; Pred. No. 1.41e-41;
Matches 97; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Db 1 elqmtgppsslsaslgervsltrcraqdigslnwlgdpdgtlkrllyatssidsyvk 60
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 21 DIQMTQSPSSISASLGVRSLTCRASQDIGINLHMQDEPDGTRKRLIYATSSLSGSGVPK 80
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 rfsgsrsgsdysltsslsesedfvdyclygasspwtffgggtklleikra 109
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 81 RFSGRSGSDYSLTSSLSSEDFVAYVYCLOYASSPYTFGGGTKLEIKR 129

RESULT 11
ID R39571 standard; Protein; 534 AA.
AC R39571;
DE 07-FEB-1994 (first entry)
DE Sequence of G-FIT.
KW Tumour antigen; c-erbB-2; G-FIT.
OS Synthetic.
PN W09316185-A.
PD 19-AUG-1993.
PF 05-FEB-1993; U01055.
PR 06-FEB-1992; US-831967.
PA (CETU) CETOUS ONCOLOGY CORP.
PI (CREA) CREATIVE BIOMOLECULES INC.
PI Houston IL, Huston JS, Oppermann H, Ring DB;
DR WPI; 93-272889/34.
DR N-PSDB; Q46086.
PT New single chain Fv polypeptide binding to C-erbB-2 tumour
PT antigen - for imaging or treating breast or ovarian cancer etc.
PS Example; pages 65-68; 87pp: English.
CC C-erbB-2 refers to a protein antigen expressed on the surface of
CC tumour cells, such as breast and ovarian tumour cells, which is an
CC approx. 200,000 mol. wt. acidic glycoprotein having an isoelectric
CC pt. of about 5.3 (see Q46083, R39568).
SQ Sequence 534 AA;

Query Match 67.5%; Score 688; DB 8; Length 534;
Best Local Similarity 89.1%; Pred. No. 1.41e-41;
Matches 98; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Db 425 d1qmtgppsslsaslgervsltrcraqdigslnwlgdpdgtlkrllyatssidsyvk 484
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 21 DIQMTQSPSSISASLGVRSLTCRASQDIGINLHMQDEPDGTRKRLIYATSSLSGSGVPK 80
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 485 rfsgsrsgsdysltsslsesedfvdyclygasspwtffgggtklleikrad 534
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 81 RFSGRSGSDYSLTSSLSSEDFVAYVYCLOYASSPYTFGGGTKLEIKRAD 130

RESULT 12
ID R15321 standard; Protein; 144 AA.
AC R15321;

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n.a. database search, using Smith-Waterman algorithm

Sat Apr 17 13:59:22 1999; MasPar time 710.56 Seconds

generated.

TACCCCGGGGACGACTCTA.....GTGGTAGGTCATTCGAACCC

TABLE default

Database 0; Query 0

5023357 seqs, 1181590623 bases x 2

Existing first 45 summaries

jenbank110

33:gb_un 34:gb_v1

mean 10.047; variance 4.775; scale 2.104

ved by analysis of the total score distribution.

SUMMARIES

Accession	Length	DB	ID	Description	Pred. No.
U00001.1	390	29	MUSKCC	Mus musculus immunoglobulin heavy chain constant region 1	1,22e-2870
U00001.1	381	29	AF054508	Mus musculus dcm1 anti-CD4	7.31e-2711
U00001.1	381	29	AF054545	Mus musculus dca anti-CD4	2.62e-2657
U00001.1	381	29	AF054510	Mus musculus 6c9 monoclonal antibody	9.33e-2646
U00001.1	380	29	MMIGV51	M. musculus mRNA for Ig M. musculus	1.13e-2488
U00001.1	381	29	MMIGV2	M. musculus mRNA for Ig M. musculus	2.35e-2433
U00001.1	383	29	MUSIGKMA	Mouse Ig active kappa chain	1.07e-2400
U00001.1	684	29	MUSIGKAC1	Mouse Ig kappa active chain	8.21e-2400
U00001.1	405	29	AB016620	Mus musculus mRNA for part of the murine genome	6.31e-2393
U00001.1	685	29	MMIK7	Mus musculus (cell line)	4.85e-2338
U00001.1	324	29	MUSK	Mus musculus (cell line)	1.69e-2334
U00001.1	739	22	AF007991	Sequence 5 from patent	1.29e-2333
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14	301	MMUS5551	Mus musculus anti-DNA	7.62e-223
15	295	103643	Sequence 4 from Patent	1.55e-223
16	295	107835	Sequence 4 from Patent	1.55e-223
17	293	324	Mus Ig germline chain	9.07e-222
18	288	MUSIGLAF	Mus Ig kappa-chain m	2.38e-222
19	286	MMUS8675	Mus musculus anti-DNA	1.39e-221
20	285	MMUS5585	Mus musculus anti-DNA	1.06e-221
21	283	MDICKVS	M.domesticus Igk varia	6.21e-221
22	281	AF003293	M.musculus Ig kappa	3.62e-221
23	281	MUSIGKVC	Mus Ig kappa germlin	3.62e-221
24	281	MMIGK3	Murine kappa-immunogl	3.62e-221
25	280	MMUS5098	Mus musculus anti-Pseu	2.76e-221
26	279	MMUS3KAF	Mus musculus Ig active	2.11e-221
27	278	MMIGLAF	M.musculus Ig1, light	1.61e-221
28	275	MUSIGKLV	Mouse IgMk rearranged	7.14e-220
29	274	MMUS8676	Mus musculus anti-DNA	5.44e-220
30	270	MMUS29617	Mus musculus anti-DNA	1.83e-220
31	270	MMU622776	Mus musculus immunogl	1.83e-220
32	269	MUSIGKAE	mouse Ig kappa unprod	1.39e-220
33	269	MMIG04	Mus pseudogene for k	1.39e-220
34	265	MMVNRB1	M.musculus mRNA for Ig	4.66e-220
35	263	AF003299	Mus musculus IgG kappa	2.69e-199
36	263	AF003294	Mus musculus Ig kappa	2.69e-199
37	262	569053	Ig V kappa -anti p-1it	2.05e-199
38	261	AF003301	Mus musculus IgG kappa	1.55e-199
39	257	MMU30236	Mus musculus anti-DNA	5.15e-199
40	256	AF003291	Mus musculus IgG kappa	3.91e-199
41	256	AI18393	Artificial sequences v	3.91e-199
42	255	MMIG15K	Mouse mAb-15c5 mRNA fo	3.91e-199
43	254	MMIGKGI1	Mouse mRNA for GAT (HP	2.24e-199
44	253	AF023475	Mus musculus anti-pneu	1.70e-188
45	252	MMIGK42	Mouse mRNA for GAT (HP	1.29e-188

ALIGNMENTS

```

FEATURES             1
LOCUS                MUSKICC      390 bp      mRNA           ROD       24-JUL-1997
DEFINITION          Mus musculus immunoglobulin kappa chain mRNA, 5' end of cds.
ACCESSION            L41880
NID                  g798810
KEYWORDS             Immunoglobulin kappa chain.
SOURCE              Mus musculus
ORGANISM             Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
                    Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                    Murinae; Mus.
REFERENCE            1 (bases 1 to 390)
AUTHORS             Asakura,K., Miller,D.J., Pogulis,R.J., Pease,L.R. and Rodriguez,M.
TITLE               Oligodehydrocyte-reactive OL, OA, and HNK-1 monoclonal antibodies
                   are encoded by germ-line immunoglobulin genes
JOURNAL             Brain Res. Mol. Brain Res. 34 (2), 283-293 (1995)
MEDLINE             96363014
REFERENCE            2 (bases 1 to 390)
AUTHORS             Asakura,K.
TITLE               Direct Submission
JOURNAL             Submitted (24-JUL-1997) Immunology, Mayo Clinic, 200 First Street
                   SW, Rochester, MN 55905, USA
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 QY 361 GGGACCAAGCTGGAATTAACCG 384
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RESULT 2
 LOCUS AF045508 381 bp mRNA ROD 28-FEB-1998
 DEFINITION Mus musculus dc10 anti-poly(dc) monoclonal antibody kappa light
 chain variable region, (Igk) mRNA, partial cds.
 ACCESSION AF045508
 NID g2906099
 KEYWORDS house mouse.
 SOURCE Mus musculus
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 381)
 AUTHORS O'Connor,K.C., Farrell,T.P., Morikawa,A. and Stollar,B.D.
 TITLE Anti-DNA antibodies of normal mice immunized with poly(dc) are
 structurally similar to natural autoantibodies
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 381)
 AUTHORS O'Connor,K.C., Farrell,T.P., Morikawa,A. and Stollar,B.D.
 TITLE Direct Submission
 JOURNAL Submitted (02-FEB-1998) Biochemistry, Tufts University School of
 Medicine, 136 Harrison Avenue, Boston, MA 02111, USA
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 Db 361 GGGACCAAGCTGGAATTAAC 381
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 QY 361 GGGACCAAGCTGGAATTAAC 381
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RESULT 3
 LOCUS AF045495 381 bp mRNA ROD 28-FEB-1998
 DEFINITION Mus musculus dc4 anti-poly(dc) monoclonal antibody kappa light
 chain variable region, (Igk) mRNA, partial cds.
 ACCESSION AF045495
 NID g2906073
 KEYWORDS house mouse.
 SOURCE Mus musculus
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 381)
 AUTHORS O'Connor,K.C., Farrell,T.P., Morikawa,A. and Stollar,B.D.
 TITLE Anti-DNA antibodies of normal mice immunized with poly(dc) are
 structurally similar to natural autoantibodies
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 381)
 AUTHORS O'Connor,K.C., Farrell,T.P., Morikawa,A. and Stollar,B.D.
 TITLE Direct Submission
 JOURNAL Submitted (02-FEB-1998) Biochemistry, Tufts University School of
 Medicine, 136 Harrison Avenue, Boston, MA 02111, USA
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AUTHORS	O'Connor,K.C., Fairrell,T.P., Morikawa,A. and Stollar,B.D.			
TITLE	Direct Substitution			
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Oy	61 GACATCCAGATGACCCAGCTGCATCTCTTATCTGCTCTCTGGGAGAAAGATCAGT 120			
Db	121 CTCACCTGTGGGGAGACGACGACATTTGTTAGTCTTAAGCTGGCTTCACGAGAACCA 180			
Oy	121 CTCACCTGTGGGGAGACGACGACATTTGTTAGTCTTAAGCTGGCTTCACGAGAACCA 180			
Db	181 GATGGAATATTTAAACACCTGATCTACGCCACATCCAGTATTAGATTCTGGTGTCCCAAA 240			
Oy	181 GATGGAATATTTAAACGCTGATCTACGCCACATCCAGTATTAGATTCTGGTGTCCCAAA 240			
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DEFINITION	M.musculus mRNA for Igk kappa light chain (partial) GI00P1.1.			
ACCESSION	X02177			
MID	g51894			
KEYWORDS	gamma-immunoglobulin; Ig light chain; immunoglobulin; joining region; variable region.			
SOURCE	house mouse.			

ORGANISM	Location/Qualifiers
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REFERENCE 1 (bases 1 to 380)	
AUTHORS Darsley,M.J. and Rees,A.R.	
TITLE Nucleotide sequences of five anti-lysozyme monoclonal antibodies	
JOURNAL EMBO J. 4 (2), 393-398 (1985)	
MEDLINE 85257466	
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Oy	80 CTCGATCCTCTTAATCTGCTCTGCGGAGAAAGTCAAGTCTCACTTGTGCGGCAATC 139
Db	121 AGGAATTAGTGTACTTAAGCTGGCTTCAGCAAAACAGATGGAATTAAGCC 180
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Oy	200 TGATCTAGCCGACATCCACTTAAATTCGTGGGTGCCAAAAAGTTGATGACATAGT 259
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Oy	260 CTGGGTCGATTAATCTCTCACACATCAGACGCTTGAAGTCTGAAGATTTTGACACTAAT 319
Db	301 ACTGCTACATATCTTAAATTAATTCGCGCTCAGCTTGGTGTGGGACCAAGCTGAGCTGA 360
Oy	320 ACTGCTACATATCTTAAATTAATTCGCGCTCAGCTTGGTGTGGGACCAAGCTGAGCTGA 379
Db	361 AACGGGTCGATGCTGCACCA 380
Oy	380 AACGGGTCGATGCTGCACCA 399
RESULT	6 MMIGVJ2 381 bp RNA ROD 03-FEB-1995
LOCUS	
DEFINITION	M.musculus mRNA for IgG kappa light chain (partial) GI0022.
ACCESSION	X02178
ENTRY	g51899

KEYWORDS	gamma-immunoglobulin; Ig light chain; immunoglobulin; joining region; variable region.
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryotes: mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sclurognathi; Myomorpha; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 381)
TITLE	Darsley,M.J. and Rees,A.R.
JOURNAL	Nucleotide sequences of five anti-lysozyme monoclonal antibodies
MEDLINE	EMBO J. 4 (2), 393-398 (1985)
FEATURES	85257466
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misc_feature	307..333
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Qy	80 CTCATCTCTCTTATCTGCTCTCTGAGGAAAGATCAGTCTACTTGTGGGCAATC 139
Db	122 AAGAAATAGAGGTACTTAAGTGGCTTCAGCAAAACCAGATGAGAACTTTAAAGCC 181
Qy	140 AGGACATTGGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 199
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Qy	380 AACGGCTGATGTCGACCA 399
RESULT	7
LOCUS	MUSIGKMA 383 bp mRNA ROD 15-MAR-1989

SEGMENT	SOURCE
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ORGANISM	Mus musculus
	Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 684) Seidman,J.G., Max,E.E. and Leder,P.
AUTHORS	A kappa-immunoglobulin gene is formed by site-specific recombination without further somatic mutation
TITLE	Nature 280 (5721), 370-375 (1979)
JOURNAL	Nature 280 (5721), 370-375 (1979)
MEDLINE	79221900
REFERENCE	2 (sites) Queen,C. and Baltimore,D.
REFERENCE	Immunoglobulin gene transcription is activated by downstream sequence elements
TITLE	Cell 33 (3), 741-748 (1983)
JOURNAL	Cell 33 (3), 741-748 (1983)
MEDLINE	83259260
COMMENT	[2] sites; comment. this sequence is a productively rearranged kappa ig from myeloma mopc41. the conflicts noted in the sites table refer to the published differences between the germline and active genes. they are probably typographical errors since [1] says that no somatic mutation has occurred after recombination. j.g. seidman (personal communication) said that the published germline sequence is correct <musigkvc>. [2] finds that deletion of 1.3kb 5' to the constant region exon results in a lowered rate of transcription and an altering of the site of transcription initiation. the deletion moves transcription initiation from approximately 30 bp 5' to the initiation codon to about 20 bp 5'. for part of the vk41 constant gene and part of the 3' flank see <musigkac> and <musigkac> respectively. for the germline joining j1 region see <musigjcz>. for other rearranged kappa genes see loci beginning <musigke>, and for germline kappa variable genes see loci beginning <musigkv>. in the sites table cdr-complementarity determining region and fr-framework region.
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Query Match	71.3%; Score 310; DB 29; Length 684; Best Local Similarity 96.1%; Pred. No. 8, 21e-240;
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Db 360	AGAAGAGTACGATCTACTGTGGGGCAAGTACAGGACATGTGTAGTACTGCTTAACTGGCT 419
Db 108	ACAAAGAGTACGATCTACTGTGGGGCAAGTACAGGACATGTGTATTAACCTTAACATTTGGCT 167
Db 420	TCACAGAGAACCCAGATGAACTATTAAAGGCTGATCTACGGCCACATCCAGTTAGATTC 479

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QY 288 CAGCCTTGAGCTGAAGATTTGTAGTATTAAGTCTAGCAATATGCTAGTCCCGT 347
Db 600 GAGCCTTGAGCTGAAGATTTGTAGTATTAAGTCTAGCAATATGCTAGTCCCGT 635
QY 348 CAGCCTTGAGCTGAAGATTTGTAGTATTAAGTCTAGCAATATGCTAGTCCCGT 383

RESULT 9
LOCUS AB016620 405 bp mRNA ROD 06-AUG-1998
DEFINITION Mus musculus mRNA for Immunoglobulin light chain variable region, partial cds.
ACCESSION AB016620
KEYWORDS 9393670
SOURCE Immunoglobulin light chain variable region.
ORGANISM Mus musculus cell_line:FU-MK-1 hybridoma cDNA to mRNA.
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Euteria;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (sites)
AUTHORS Arakawa,F., Yamamoto,T., Kanda,H., Matsubae,T. and Kuroki,M.
TITLE Cloning and sequencing of cDNAs encoding the variable domains of monoclonal antibody FU-MK-1 specific for a transmembrane carcinoma-associated antigen, and construction of a mouse/human chimeric antibody
JOURNAL Unpublished (1998)
REFERENCE 2 (bases 1 to 405)
AUTHORS Arakawa,F.
TITLE Direct Submission
JOURNAL Submitted (30-JUL-1998) to the DDBJ/EMBL/GenBank databases. Funiko
Arakawa, School of Medicine, Fukuoka University, First Department
of Biochemistry, 7-45-1 Nanakuma, Jonan-ku, Fukuoka, Fukuoka
814-80, Japan (E-mail:arakawa@sat.fukuoka-u.ac.jp,
Tel:092-801-1011(ex.3246), Fax:092-801-3600)
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primer_bind
393..405
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intron
393..405
BASE COUNT 98 a 100 c 97 g 110 t
ORIGIN
Query Match 71.0%; Score 309; DB 29; Length 405;
Best Local Similarity 90.3%; Pred.No.6,31e-239;
Matches 346; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

Db 11 ATGAGGGCCCTGCTCAGATTCCTGGCTTCTGTTGCTCAGTATTAGATGT 70
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QY 1 ATGGGGGCCCTGCTCAGATTCCTGGGTTCTGTTGCTTGTTCAGGATACAGATGT 60
Db 71 GACATCAAGATGACCCAGTGCATCTCTTATCTGCTCTGGAGAAAGTCACT 130
QY 61 GACATCCAGATGACCCAGTGCATCTCTTATCTGCTCTGGAGAAAGTCACT 120
Db 131 CTCAGTGTGGGCAAGTCAGGAATTAAGTGTACTTAAGTGTCTGACGCAAAAACA 190
QY 121 CTCAGTGTGGGCAAGTCAGGAATTAAGTGTACTTAAGTGTCTGACGCAAAAACA 180
Db 191 GATGAACCTGTTAAACCCCTGATCTAGCCGATCCACTTACATTCCTGTTGCCAAA 250
QY 181 GATGAACCTGTTAAACCCCTGATCTAGCCGATCCACTTACATTCCTGTTGCCAAA 240
Db 251 AGTTTCAGTGGCAGTAGGTCGGTCAAGTATTCCTACACATCAGACAGCTTGAAGTCT 310
QY 241 AGTTTCAGTGGCAGTAGGTCGGTCAAGTATTCCTACACATCAGACAGCTTGAAGTCT 300
Db 311 GAGATTTTGACAGCTATTTACTGCTACAGATGCTGATCCGTGGAGTTCGGTGA 370
QY 301 GAGATTTTGACAGCTATTTACTGCTACAGATGCTGATCCGTGGAGTTCGGAGG 360
Db 371 GGCACCAAGCTGGAATCAACG 393
QY 361 GGCACCAAGCTGGAATCAACG 383

RESULT 10
LOCUS NMIGK7 685 bp DNA ROD 21-NOV-1994
DEFINITION Part of the murine gene for kappa-immunoglobulin leader peptide and variable part (cell line MOPC41).
ACCESSION V00808 J00565
KEYWORDS 952134
SOURCE differentiated gene; Ig kappa light chain; Immunoglobulin.
ORGANISM Mus musculus
Eukaryota; Eukaryotes; Metazoa; Chordata;
Vertebrata; Euteria; Rodentia; Sciurognathi; Myomorpha; Muridae;
Murinae; Mus.
REFERENCE 1 (bases 1 to 685)
AUTHORS Seidman,J.G., Max,E.E. and Leder,P.
TITLE A kappa-immunoglobulin gene is formed by site-specific
recombination without further somatic mutation
JOURNAL Nature 280 (5721), 370-375 (1979)
MEDLINE 79221900
COMMENT KST MMU. IGHAP.MOPC41.
FEATURES
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/organism="Mus musculus"
/db_xref="taxon:10090"
120..173
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120..173
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302..637
exon
302..637
BASE COUNT 164 a 158 c 146 g 217 t
ORIGIN
Query Match 70.8%; Score 308; DB 29; Length 685;
Best Local Similarity 95.8%; Pred.No.4,85e-238;
Matches 322; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Db 301 AGTACCAAGATGTACATCCAGATGACCCAGTCCATCTCTTATCTGCTTGGG 360
QY 48 AGTACCAAGATGTACATCCAGATGACCCAGTCCATCTCTTATCTGCTTGGG 107
Db 361 AGAAGAGTCAAGTCTCACTGTGCGGCAAGTCAAGCAATGTGTAGTCACTAACTGGCT 420
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QY 108 ACAAGAGTCAAGTCTCACTGTGCGGCAAGTCAAGCAATGTGTAGTCACTTGGCT 167
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Db 421 TCAGCAGGAACGATGAGTAAAGCCGATCTACGCCACATCCAGTTAGATTC 480
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Qy 168 TCAGCAGGAACGATGAGTAAAGCCGATCTACGCCACATCCAGTTAGATTC 227
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Db 481 TGGTGTCGCCAAAGGTTGAGTGGCAGTAGTGGTGCAGTATTTCTCTCCATCAG 540
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Qy 228 TGGTGTCGCCAAAGGTTGAGTGGCAGTAGTGGTGCAGTATTTCTCTCCATCAG 287
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Db 541 CAGCCTTGAGTCTGAAGATTTGTAGACTATTAACAAATATGCTAGTTCCGCTG 600
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Qy 288 CAGCCTTGAGTCTGAAGATTTGTAGACTATTAACAAATATGCTAGTTCCGCTG 347
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Db 601 GAGCTCGGTGGAGGACCAAGCTGGAATCAACG 636
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Qy 348 CAGCTTCGGAGGGGGGACCAAGCTGGAATCAACG 383
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RESULT 11
LOCUS MUSX 324 bp mRNA
DEFINITION Mus musculus (cell line C3H/F2-15) chromosome 6 anti-DNA antibody
ACCESSION L48667
NID 91050293
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Eukaryotae; mitochondria eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE 1 (bases 1 to 324)
AUTHORS Mloch, M.K., Alexander, A.L., Pippen, A.M., Pisetsky, D.S. and Gillespie, G.S.
TITLE Differences in V kappa gene utilization and VH CDR3 sequence among anti-DNA from C3H-1pr mice and lupus mice with nephritis
JOURNAL Eur. J. Immunol. 26 (9), 2225-2233 (1996)
MEDLINE 96409289
FEATURES
source Location/Qualifiers
1..324
/organism="Mus musculus"
/strain="C3H/HeJ-1pr/1pr"
/db_xref="taxon:10090"
/cell_line="C3H/F2-15"
/cell_type="hybridoma"
/tissue_type="spleen"

BASE COUNT 83 a 76 c 87 t 1 others
ORIGIN

Query Match 69.9%; Score 304; DB 28; Length 324;
Best Local Similarity 96.9%; Pred. No. 1,696-234;
Matches 313; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 361 GGGACCAAGCTGGAAATTAACG 383
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RESULT 12
LOCUS AR007981 739 bp DNA
DEFINITION Sequence 5 from patent US 5753204.
ACCESSION AR007981
NID 93967090
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 739)
AUTHORS Huston, J.S., Huston, L.L., Ring, D.B. and Oppermann, H.
TITLE Biosynthetic binding proteins for immunotargeting
JOURNAL Patent: US 5753204-A 5 19-MAY-1998;
FEATURES
source Location/Qualifiers
1..739
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BASE COUNT 188 a 177 c 181 g 193 t
ORIGIN

Query Match 69.7%; Score 303; DB 22; Length 739;
Best Local Similarity 95.2%; Pred. No. 1,296-233;
Matches 319; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Db 395 GATCCATATTCAGATGACCAAGTCCATCCCTTATCTGCTCTGGAGAAAG 454
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Qy 56 GATGTGACATCCAGATGACCAAGTCCATCCCTTATCTGCTCTGGAGAAAG 115
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Db 455 TCAGTCTCACTTTCGGGCAAGTCAGACATTGTAATAGCTTACCTGCTTCAGCAG 514
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Qy 116 TCAGTCTCACTTTCGGGCAAGTCAGACATTGTAATAGCTTACCTGCTTCAGCAG 175
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Db 515 AACCAATGGAATATTAACGCTATCTAGCCACATCCATTTAGATTCGGTGC 574
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Qy 176 AACCAATGGAATATTAACGCTATCTAGCCACATCCATTTAGATTCGGTGC 235
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Db 575 CCAAAAGTTCAGTGGCAGTCGCTGGGTCAGATATCTCCACATCAGTAGCTTG 634
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Qy 236 CCAAAAGTTCAGTGGCAGTCGCTGGGTCAGATATCTCCACATCAGTAGCTTG 295
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Db 635 AGCTGAAGATTTTGTAGTCTATTAAGTCTTACATATGATATTTTCGTACAGCTTC 694
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Qy 296 AGCTGAAGATTTTGTAGTCTATTAAGTCTTACATATGATATTTTCGTACAGCTTC 355
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Db 695 GAGGGGGACCAACTGGAAATTAACGGGCTGAT 729
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Qy 356 GAGGGGGACCAACTGGAAATTAACGGGCTGAT 390
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RESULT 13
LOCUS I23446 739 bp DNA
DEFINITION Sequence 5 from patent US 5534254.
ACCESSION I23446
NID 91603316
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 739)
AUTHORS Huston, J.S., Huston, L.L., Ring, D.B. and Oppermann, H.
TITLE Biosynthetic binding proteins for immunotargeting
JOURNAL Patent: US 5534254-A 5 09-JUL-1996;
FEATURES
source Location/Qualifiers
1..739
/organism="unknown"

BASE COUNT 188 a 177 c 181 g 193 t
ORIGIN

Query Match 69.7%; Score 303; DB 22; Length 739;
Best Local Similarity 95.2%; Pred. No. 1,296-233;

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Db	395	GATCCGATATTCAGATGACCCAGTCTCCATCTCTTATCTGCTCTCTGAGGAAAG	454						
Qy	56	GATGTGACATCCAAATGACCCAGTCTCCATCTCTTATCTGCTCTCTGAGCAAG	115						
Db	455	TCAGTTCACCTGTGCGGCAAGTACGACATTGGTATAGTTTAACTCGCTTACAGG	514						
Qy	116	TCAGTCTCAGTGTGCGGCAAGTACGACATTGGTATTAATCTTCAATGGCTTACAGG	175						
Db	515	AACCAAGTGAACATTATTAACGCTGATCTACGGCACATCCAGTTTATGATCTGTGTGCC	574						
Qy	176	AACCAAGTGAACATTATTAACGCTGATCTACGGCACATCCAGTTTATGATCTGTGTGCC	235						
Db	575	CCAAAAGGTCAGTGGCAGTGGGTCTGGGTGAGATTATCTCTACCATCAGTAGCCTTG	634						
Qy	236	CCAAAAGGTCAGTGGCAGTGGGTCTGGGTGAGATTATCTCTACCATCAGTAGCCTTG	295						
Db	635	AGTCTGAAGATTTTGTAGTCTATTACTGTCTACAAATATGCTATTTTTCCGTACAGTTTG	694						
Qy	296	AGTCTGAAGATTTTGTAGTCTATTACTGTCTACAAATATGCTATTTTTCCGTACAGTTTG	355						
Db	695	GAGGGGGGACCACTGGGAATTAAGAGGGGTGAT	729						
Qy	356	GAGGGGGGACCACTGGGAATTAAGAGGGGTGAT	390						

RESULT	14			
LOCUS	MMU55591	328 bp	mRNA	06-MAR-1997
DEFINITION	Mus musculus anti-DNA immunoglobulin light chain 1g9, antibody 363s.73, partial cds.		ROD	
ACCESSION	U55591			
NID	g1870297			
KEYWORDS				
SOURCE	house mouse.			
ORGANISM	Mus musculus			
	Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE	1 (bases 1 to 328)			
AUTHORS	Krishnan,M.R., Jou,N.-T. and Marion,T.N.			
TITLE	Correlation between somatically derived VH-CD3 structures and specificity for DNA among autoimmune antibodies to DNA			
	J. Immunol. (1997) In press			
JOURNAL	2 (bases 1 to 328)			
REFERENCE	Marion,T.N.			
FILE	Direct Submission			
AUTHORS	Submitted (18-APR-1996) Tony N. Marion, Dept. of Microbiology/Immunology, University of Tennessee, 858 Madison Ave			
JOURNAL	Memphis, TN 38163, USA			

FEATURES	
source	Location/Qualifiers
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/cell_type="hybridoma"	
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/codon_start=2	
/product="anti-DNA immunoglobulin light chain IgG"	
/db_xref="PID:g1870298"	
/translation="ITQSPKXISASIGSERVSLTCRASQIGSLMNLQEPDPTGIK IYITSSLDSCVPRKRFSGSRSGSDYSLTISLSESDVVDYICLIQYASSPPTFGGTX IKRADAA"	
BASE COUNT	81 a 80 c 78 g 85 t 4 others
ORIGIN	
Query Match	69.2% Score 301, DB 29, Length 328;
Best Local Similarity	95.4% Pred. No. 7,62e-232;
Matches 311; Conservative	1; Mismatches 14; Indels 0; Gaps 0;

Db	3	TGACCAGTCTCCATCCMCCTTATCTGCTCTCTGGGAGAAAGTAGTCACTACTTGTG	62
Qy	71	TGACCAGTCTCCATCCCTCTTATCTGCTCTCTGGGAGAAAGTAGTCACTACTTGTG	136
Db	63	GGGCAAGTCAGAGACATGGTGTGTAGTCTTAAACGTGGCTTCAACAGAACCCAGATGGACTA	122
Qy	131	GGGCAAGTCAGAGACATGGTGTGTGTAGTCTTAAACGTGGCTTCAACAGAACCCAGATGGACTA	190
Db	123	TTAAAGCGCTATCTACGCCATCCATCCAGTTAGATCTGGGTGCCCAAAAGTTTCAGTG	182
Qy	191	TTAAAGCGCTATCTACGCCATCCATCCAGTTAGATCTGGGTGCCCAAAAGTTTCAGTG	250
Db	183	GCAGTAGTCTGGGTCCAGATTATTTCTCTCNCCATCAGACAGCTTGAAGTCAATTTG	242
Qy	251	GCAGTAGTCTGGGTCCAGATTATTTCTCTCNCCATCAGACAGCTTGAAGTCAATTTG	310
Db	243	TAGACTATTAAGTCTACAAATATCTCTAGTTCTCTCCACAGTTGGAGGGGGGACCAAGC	302
Qy	311	TAGACTATTAAGTCTACAAATATCTCTAGTTCTCTCCACAGTTGGAGGGGGGACCAAGC	370
Db	303	TGAAATTTAAACGGGCTGATGCTGTCA	328
Qy	371	TGAAATTTAAACGGGCTGATGCTGTCA	396

	RESULT	15		PAT	05-MAR-1993
LOCUS	103643	324 bp ss-DNA			
DEFINITION	Sequence 4 from Patent US 4642334.				
ACCESSION	J03643				
NID	g268618				
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 324)				
TITLE	Moore,K.W. and Zaffaroni,A.				
JOURNAL	Hybrid DNA prepared binding composition Patent: US 4642334-A 4 10-FEB-1987; DNAX Research Institute of Molecular and Cellular Biology, Inc., Palo Alto, CA				
FEATURES	Location/Qualifiers				
source	1..324				
BASE COUNT	82 a /organism="unknown"				
ORIGIN	80 c 75 g 87 t				
Query Match	67.8%	Score 295;	DB 22;	length 324;	
Best Local Similarity	95.7%;	Pred. No. 1.55e+226;			
Matches 309; Conservative	0;	Mismatches 14;	Indels 0;	Gaps 0;	

Db	1	GACATCCAGATGACCAGTGTCCATCTCTCTTACTCTCCCTCTGCGGAGAAAGAGTAGT	60
Qy	61	GACATCCAGATGACCAGTGTCCATCTCTCTTACTCTCCCTCTGCGGAGAAAGAGTAGT	120
Db	61	CTCACTGTGGGCCCAAGTCCAGGACATTGGTAGTAGCTTAAACTGGCTTCAGCAGGAACCA	120
Qy	121	CTCACTGTGGGCCCAAGTCCAGGACATTGGTAGTAGCTTAAACTGGCTTCAGCAGGAACCA	180
Db	121	GATGAGAACTATTAAACCCGATGCTACGCCACATCCAGTTAGATTCGTGTGCCCAA	180
Qy	181	GATGAGAACTATTAAACCCGATGCTACGCCACATCCAGTTAGATTCGTGTGCCCAA	240
Db	181	AGGTTCAAGTGGCAGTAGGCTGGGCTCAGATTATTCCTCCACATCAGACACCTTGAAGTCT	240
Qy	241	AGGTTCAAGTGGCAGTAGGCTGGGCTCAGATTATTCCTCCACATCAGACACCTTGAAGTCT	300
Db	241	GAAATTTTGTAGACTTACTGTCTACAAATATGCTAGTCTCCGTGACGTTGGGTGA	300
Qy	301	GAAATTTTGTAGACTTACTGTCTACAAATATGCTAGTCTCCGTGACGTTGGGTGA	360
Db	301	GGCACCAGCTGGAATCAACG	323
Qy	361	GGCACCAGCTGGAATCAACG	385

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Search completed: Sat Apr 17 14:27:52 1999
Job time : 1710 secs.

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RESULT	3	458 bp	PAT	14-NOV-1994
LOCUS	105921	458 bp		
DEFINITION	Sequence 37 from Patent EP 0274394.			
ACCESSION	105921			
NID	9590876			
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	1 (bases 1 to 458)			
AUTHORS	Robinson,R.R., Liu,A.Y., Hellstrom,K.E., Hellstrom,I. and Ledbetter,J.A.			
TITLE	Chimeric antibody with specificity to human B cell surface antigen			
JOURNAL	Patent: EP 0274394-A2 37 13-JUL-1988;			
FEATURES	Location/Qualifiers			
source	1..458			
BASE COUNT	113 a 120 c 112 g 113 t			
ORIGIN				
Query Match	68.1%; Score 314; DB 22; Length 458;			
Best Local Similarity	94.6%; Pred. No. 2,71e-216;			
Matches	333; Conservative 0; Mismatches 19; Indels 0; Gaps 0;			
Db	39 ATGGGATTGACGACGATCTTTCTCTCTCTCTCTGTCAGTACTACAGGTGTCACCTCCAG 98			
QY	1 ATGGAATGACGCTGGGCTCTTCTCTCTCTCTCTCTGTCATTAACACAGGTGTCACCTCCAG 60			
Db	99 GCTTATCTAAGAGCTCTGGGCTGAGCTGGTGAGCGCTGGGGCTCTGATGTAATATGTC 158			
QY	61 GCTTATCTAAGAGCTCTGGGCTGAGCTGGTGAGCTCTGGGGCTCTGTAAGATGTC 120			
Db	159 TGCAGGCTTCTGGCTACACATTTTACACAGTTTACATATGCACTGGGTAAACAGACACT 218			
QY	121 TGCAGGCTTCTGGCTACACATTTGACAGCTTTCATATGCACTGGGTAAACAGACACT 180			
Db	219 AGACAGGCTCTGAATGATTTGAGCTATTTATCCAGGAATATGATATCTTCTACAT 278			
QY	181 GACAGGCTCTGAATGATTTGAGCTATTTTCTCGAAATATGATATCTTCTACAT 240			
Db	279 CAGAGTTCAAGGCGACACACTGACTGTGACAAATCTCCAGACAGCTTACATG 338			
QY	241 CAGAGTTCAAGGCGACAGCTTATGATGTGACACACATCTCCAGACAGCTTACATG 300			
Db	339 CAGCTCAGAGCTGACATCTGAAGACTCTGGGCTATTTCTGTGCAAGAG 390			
QY	301 CAGATCAGACGCTGACATCTGAAGACTCTGGGCTATTTCTGTGCAAGAG 352			
RESULT	4	458 bp	PAT	14-NOV-1994
LOCUS	108811	458 bp		
DEFINITION	Sequence 12 from Patent WO 8804936.			
ACCESSION	108811			
NID	9588489			
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	1 (bases 1 to 458)			
AUTHORS	Robinson,R.R., Liu,A.Y., Hellstrom,K.E., Hellstrom,I. and Ledbetter,J.A.			
JOURNAL	Patent: WO 8804936-A 12 14-JUL-1988;			
FEATURES	Location/Qualifiers			
source	1..458			
BASE COUNT	113 a 120 c 112 g 113 t			

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Qy	118	TCGCGAAGGCTTCTGGCTACACATTGACCAGTTCAAATGCTACCTGGGTAAAGCAGACA	177
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Qy	178	CTGTGACAGAGGCCCTGGAAATGATTTGGAAATATTTTTTCCGTGGAAATGGTATCTTACTTAC	237
Db	181	AATCAGAAGTTTCAAGGGCAAGGCCACACTGACTGTATGACAAATCTCTCCAGCACAGCTTAC	240
Qy	238	AATCAGAAGTTTAAAGGGCAAGGCCCTATTGACTGCGACAGACATCTCTCCAGCACAGCTTAC	297
Db	241	ATGCAGTCTACAGGCTTGACATCTGGAAGACTGTGCGTATATTTCTGTGCAAGAGGGGAT	300
Qy	298	ATGCAGATTCAGACGCTTGACATCTGGAAGACTGTGCGTATATTTCTGTGCAAGAGGGAAC	357
Db	301	TATCGGCTGTATTAAGACTCTGGGGGCAAGGCAACACTCTACAGTCTCTCTCA	354
Qy	358	TGGGAGGCTGCTCTGCACTACTGTGGGTCAAGGAACCTCAGTACCGGTCTCTCTCA	411

RESULT	8	357 bp	RNA	ROD	07-JAN-1997
LOCUS	MUS				
DEFINITION	Mus musculus (cell line C3H/Fe-20)			chromosome 12 anti-DNA antibody	
ACCESSION	heavy chain mRNA.				
NID	148668				
KEYWORDS	g1050294				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	1 (bases 1 to 357) Wloch,M.K., Alexander,A.L., Pippen,A.M., Pisetsky,D.S. and Gilkeson,G.S.				
TITLE	Differences in V kappa gene utilization and VH CDR3 sequence among anti-DNA from C3H-Ipr mice and lupus mice with nephritis				
JOURNAL	Eur. J. Immunol. 26 (9), 2225-2233 (1996)				
MEDLINE	96409289				
FEATURES	Location/Qualifiers				
SOURCE	1..357				
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	/cell_line="C3H/Fe-20"				
	/cell_type="hybridoma"				
	/tissue_type="spleen"				
BASE COUNT	94 a 88 c 89 g 85 t 1 others				
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Best Local Similarity	91.9%; Pred. No. 2,056-193;				
Matches	328; Conservative 0; Mismatches 26; Indels 3; Gaps 1;				
Db	1 CAGGCTTAATACAGACAGTCTGGGCGCTGAGGCGCTGAGGCGCTCAGTGAAGATG 60				
QY	58 CAGGCTTAATACAGACAGTCTGGGCGCTGAGGCGCTGAGGCGCTCAGTGAAGATG 117				
Db	61 TCCGCGAAGGCTCTGGCTACACATTACCACCTTCACCAATATGCCATGGGTAACAGACGA 120				
QY	118 TCCGCGAAGGCTCTGGCTACACATTACCACCTTCACCAATATGCCATGGGTAACAGACGA 177				
Db	121 CCTAGACAGGCGCTGGAATGATGGAGCTATTATCCAGAAATGATGATCTCCATC 180				
QY	178 CCTAGACAGGCGCTGGAATGATGGAGCTATTATCCAGAAATGATGATCTCCATC 237				
Db	181 AATCAGAACTTCAGAGGCGCAAGGCCACACCTGACTGTAGCAAAATCCTCCAGACAGCTAC 240				
QY	238 AATCAGAACTTCAGAGGCGCAAGGCCCTCATGACTGCAGACACATCCTCCAGACAGCTAC 297				
Db	241 ATGAGAGTCAGACGCTGACATCTGAAGCTCTGGGGCTCATTTCTGTGCAGAACTCAT 300				
QY	298 ATGAGAGTCAGACGCTGACATCTGAAGCTCTGGGGCTCATTTCTGTGCAGAAAGGAGAC 357				

RESULT	9	355 bp	RNA	ROD	20-DEC-1996
LOCUS	Musculus musculus	355 bp	RNA	ROD	20-DEC-1996
DEFINITION	M. musculus mRNA for rearranged Ig heavy chain V region (J588 family; 129Md.4/c).				
ACCESSION	Z73342				
NID	g1322170				
KEYWORDS	antigen receptor; diversity region; immunoglobulin; immunoglobulin heavy chain; immunoglobulin superfamily; joining region; variable region.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
TITLE	1 (bases 1 to 355)				
REFERENCE	Texido,G., Jacobs,H., Meiering,M., Kuhn,R., Roes,J., Muller,W., Giffilian,S., Fujiwara,H., Kikutani,H., Yoshida,N., Amakawa,R., Benoist,C., Mathis,D., Kishimoto,T., Mak,T.W. and Rajewsky,K. Somatic Hypermutation occurs in B cells of Tdt, CD23, IL-4, Igd and CD30 deficient mouse mutants				
AUTHORS	Unpublished				
TITLE	2 (bases 1 to 355)				
REFERENCE	Mueller,W.				
AUTHORS	Direct Submission				
TITLE	Submitted (14-MAY-1996) Mueller W., Institute for Genetics at the University of Cologne, Weyerl 121, Cologne 50931, Germany				
REFERENCE	3 (bases 1 to 355)				
AUTHORS	Texido,G., Jacobs,H., Meiering,M., Kuhn,R., Roes,J., Muller,W., Giffilian,S., Fujiwara,H., Kikutani,H., Yoshida,N., Amakawa,R., Benoist,C., Mathis,D., Kishimoto,T., Mak,T.W. and Rajewsky,K. Somatic hypermutation occurs in B cells of terminal deoxynucleotidyl transferase-, CD23-, interleukin-4-, Igd- and CD30-deficient mouse mutants				
TITLE	Eur. J. Immunol. 26 (8), 1966-1969 (1996)				
REFERENCE	96350523				
AUTHORS	Automatically created by DNAPLOT version: 1.8 (1)				
TITLE	http://www.genetic.uni-koeln.de/dnaplot.				
REFERENCE	Location/Qualifiers				
AUTHORS	1..355				
TITLE	/organism="Mus musculus"				
REFERENCE	/strain="129/SV"				
AUTHORS	/note="Partial V-D-J region"				
TITLE	/db_xref="taxon:10090"				
REFERENCE	/rearranged				
AUTHORS	/cell_type="IgM/IgD positive B cells"				
TITLE	BASE COUNT				
REFERENCE	94 a 92 c 92 g 77 t				
AUTHORS	ORIGIN				
TITLE	Query Match				
REFERENCE	Best Local Similarity 89.3%; Score 279; DB 29; Length 355;				
AUTHORS	Matches 317; Conservative 0; Mismatches 38; Indels 0; Gaps 0;				
TITLE	Db				
REFERENCE	1 CAGGTCACACTGCACACGCTGGGGCTGAGCGTGAGACCTCGGGGCTCAGTGAATG 60				
AUTHORS	58 CAGGCTTATCTACACACAGCTGGGGCTAGCGTGAGAGCTCGGGGCTCAGTGAAGTG 117				
TITLE	Db				
REFERENCE	61 TCCTCAGAGGCTTCCTGGGTACACATTTCACAGTTTACATATGACATGCGGTAAAGACACA 120				
AUTHORS	118 TCCTCAGAGGCTTCCTGGGTACACATTTCACAGTTTACATATGACATGCGGTAAAGACACA 177				
TITLE	Db				
REFERENCE	121 CCTGCACAGGCGCTGGAATGATTGGAGCTATTATCCAGAAATGTGATCTTCTCTAC 180				
AUTHORS	178 CCTGCACAGGCGCTGGAATGATTGGAAATATTTTCTCGAAATGATGATCTTCTCTAC 237				
TITLE	Db				
REFERENCE	181 AATCAGAGTTCAAAAGGCAAGGCCATTCATTCAGACCAATCCTCAGACAGACCTAC 240				
AUTHORS	238 AATCAGAGTTTAAAGGCAAGGCCCTCATTCATTCAGACCAATCCTCAGACAGACCTAC 297				

Db	241	ATGACGCTCAGCAGCCTTACATCTGAGACCTCTGACGCTCTATTACTGTGCAAGAGGCTAC	300
Qy	298	ATGCAGATCACAGCAGCTTGACATCTGAACAGCTCTGGGGCTTTCTGTGCAAGAGGGAGAC	357
Db	301	TAGCGTACTACTCTTGGACTACTGGGGCCAGACACCACTCCACAGCTCCCTGAC	355
Qy	358	TGGAGGGTGTCTCTGGACTACTGGGGGTAAAGAACCTTAGTCACCGCTCTCTCAG	412

RESULT	10.
LOCUS	MMMD1C 358 bp RNA ROD 20-DEC-1996
DEFINITION	M.musculus mRNA for rearranged Ig heavy chain V region (J588 family; 129MD.01c).
ACCESSION	F73357
NID	g1322156
KEYWORDS	antigen receptor; diversity region; immunoglobulin; immunoglobulin heavy chain; immunoglobulin superfamily; joining region; variable region.
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryote; mitochondria eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 358)
AUTHORS	Texido,G., Jacobs,H., Meiering,M., Kuhn,R., Roes,J., Muller,W., Giffillan,S., Fujiswara,H., Kikutani,H., Yoshida,N., Amakawa,R., Benoit,C., Mathis,D., Kishimoto,T., Mak,T.W. and Rajewsky,K.
TITLE	Somatic Hypermutation occurs in B cells of Tdt, CD23, IL-4, IgD and CD30 deficient mouse mutants
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 358)
AUTHORS	Mueller,M.
TITLE	Direct Submission
JOURNAL	Submitted (14-MAY-1996) Mueller W., Institute for Genetics at the University of Cologne, Weyertal 121, Cologne 50931, Germany
REFERENCE	3 (bases 1 to 358)
AUTHORS	Texido,G., Jacobs,H., Meiering,M., Kuhn,R., Roes,J., Muller,W., Giffillan,S., Fujiswara,H., Kikutani,H., Yoshida,N., Amakawa,R., Benoit,C., Mathis,D., Kishimoto,T., Mak,T.W. and Rajewsky,K.
TITLE	Somatic hypermutation occurs in B cells of terminal deoxynucleotidyl transferase-, CD23-, interleukin-4-, IgD- and CD30-deficient mouse mutants
JOURNAL	Eur. J. Immunol. 26 (8), 1966-1969 (1996)
MEDLINE	96350523
COMMENT	Automatically created by DNAPLOT version: 1.8 (1) http://www.genetik.uni-koeln.de/dnaplot .
FEATURES	Location/Qualifiers
SOURCE	1..358
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	/strain="129/SV"
	/note="partial V-D-J region"
	/db_xref="taxon:10090"
	/rearranged
	/cell_type="IgM/IgD positive B cells"
BASE COUNT	93 a 96 g 79 t
ORIGIN	

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Matches 325; Conservative	0;	Mismatches 30;	Indels 3;	Gaps 2;

Db	1	CAGGTGCACATGCACACACCTGGGGCTGAGCTGGTGAAGCCTGGGGCTCGATGAAGATG	60
Qy	58	CAGGCTTATCTACACACATCTGGGGCTAGCTGGTGAAGCTCTGGGGCTCAGTGAAGATG	117
Db	61	TCCTCAGAGGCTTCGGCTACACATTTACACAGTTACATATGCACTGGTAAAGCAGACA	120
Qy	118	TCCTCAGAGGCTTCGGCTACACATTTACACAGTTACATATGCACTGGTAAAGCAGACA	177
Db	121	CCTGCACAGGGCTTCGGATATGATGGAGCTATTATTCACAGAAATGGTATCTTCTAC	180
Qy	178	CCTGCACAGGGCTTCGGATATGATGGAAATATTTTCTCGAAATGGTATCTTCTAC	237

[illegible]

Db	121	CCTGGCAGAGGCGCTGGAAATGATTTGGAGCTATTATTATCCAGGAAATGCTATACTTCTCAG	180			
QY	178	CCTGGACAGGCGCTGGAAATGATTTGGAAATATTTTCTCGGAAATGATATACTTACTAC	237			
Db	181	AATCAGAAATTTAAAGGCGCAAGGCGCAATTCATGATCGACAGACAATTCCTCCAGCAGGCTCAG	240			
QY	238	AATCAGAAATTTAAAGGCGCAAGGCGCTCATTCATTCATTCGACAGACATTCCTCCAGCAGGCTCAG	297			
Db	241	ATGCAGATTCAGAGGCTGACATCTGAGGACNCTGGCGTATTTACTGTGCAAGACAGCAGC	300			
QY	298	ATGCAGATTCAGAGGCTGACATCTGAGGACNCTGGCGTATTTACTGTGCAAGAGGAGAAC	357			
Db	301	TCGGC --- GCGCTATGAGCTACTCTGGGGGTCAAGAGACCTCAGTACCGCTCCACAG	352			
QY	358	TGGGAGGCTGCTCTGATCTACTTGGGGGTCAAGAGACCTCAGTACCGCTCCACAG	412			
RESULT	12	AF045892	416 bp	mRNA	ROD	19-FEB-1998
LOCUS		Mus musculus	Iggb2a	heavy chain	mAb12-1A	VH domain
DEFINITION		cds.				partial
ACCESSION		AF045892				
NID		92895948				
KEYWORDS		house mouse.				
SOURCE		Mus musculus				
ORGANISM		Eukaryote; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;				
REFERENCE		Kodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS		1 (bases 1 to 416)				
TITLE		Che,Z., Olson,N.H., Mosser,A.G., Leipe,D., Rueckert,R.R.,				
JOURNAL		Baker,T.S. and Smith,T.J.				
REFERENCE		Antibody-mediated neutralization of human rhinovirus 14 explored by				
AUTHORS		means of cryo-electron microscopy and X-ray crystallography of				
TITLE		virus-Fab complexes				
JOURNAL		J. Virol. (1998) In press				
REFERENCE		2 (bases 1 to 416)				
AUTHORS		Che,Z. and Smith,T.J.				
TITLE		Direct Submission				
JOURNAL		Submitted (04-FEB-1998) Biol. Sciences, Purdue University, Lilly				
FEATURES		Hall B135, West Lafayette, IN 47907, USA				
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		<1..>416				
		/note="VH domain; binds to N1m-1A loop to neutralize human				
		rhinovirus 14"				
		/codon_start=1				
		/product="Iggb2a heavy chain mAb12-1A"				
		/db_xref="PID:g2895949"				
		/translation="VHSQGLQDSGAEIVRPGSSVKISCKASGYAESSYMMWYKQRP				
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		GNYPAMDYWGOSTSVYSSAKTAPVYPLAGSLG"				
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		ORIGIN				
		Query Match	59.7%	Score 275;	DB 29;	Length 416;
		Best Local Similarity	84.9%;	Pred. No. 1.54e-185;		
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					Indels	3;
					Gaps	2;
Db	1	GTCACATCCCAAGGGTCAAGTTCACACAGTCTTGGGCTGAGCTGCTGAGGCGCGGGTCTCTCA	60			
QY	49	GTCACATCCCAAGGGTCTTATCTACACAGTCTGGGGCTAGCGTGGAGGTCCTGGGGCGCTCA	108			
Db	61	GTGAGATTTCTCTCAAGGCTTCTGGCTATGCTACGTACGTCTCGATCGATTAAGTCGGGAT	120			
QY	109	GTGAGATTTCTCTCAAGGCTTCTGGCTACACATTTGACCACTTTCATATGCACTGGGATA	168			
Db	121	AAGCAGAGGCGCTGGACAGGGCTTTGAGTGGATTGGACAGATTTATCCTCGAGATGTGAT	180			
QY	169	AAGCAGACACTGGACAGGCGCTGGATGGATTGGAAATATTTTCTCGGAAATGTGAT	228			

[illegible]

Oy	1	ATGGAATCAGACTGGGTCTTTCTCTCTCCCTCCGTCACATAAATCAACAGTGTCCACATCCAG	60
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Oy	61	GCTATTCTTACAGACAGTCTGGGGCTGAGCTGGTAGAGTCTGGGGCTCATGTAGAATGTCC	120
Db	169	TGCAGAGCTTGCGCTAACCTTACTTACTGCCATCTGATGACACTGGGTAAACAGAGGCT	228
Oy	121	TGCAGAGCTTGCGCTAACCATTAATGACCAGTTACAAATATGACTGGGTAAACAGACACT	180
Db	229	GGACAGGCTTGTGAATGATTTGATATCACTTAATCTTAACACTGGTTATATCAATATCAAT	288
Oy	181	GGACAGGGCCCTGATGATGATTTGAATAATTTTTCTGGAATGTGGATACTTACTACAAAT	240
Db	289	CAGAACTTCAAGAGACAAGGACATTTGACTGCTCAGACAACAATCCTCCAGCACAGCTTACATG	348
Oy	241	CAGAAGTTTAAGGGCAAGGCTCATTTGACTGCTCAGACAACAATCCTCCAGCACAGCTTACATG	300
Db	349	CAACTGACCACTGATGACATCTGAGGACTCTGACGTCATTTATTTGACAAAGAGCTACTAT	408
Oy	301	CAGATCAGACACCTGATGACATCTGAAACACTCTCGGCTATTTCTGTGCAAGAGG-----	354
Db	409	AACATCAGAGGGGCTATGATGATCTAGGAGGCTAAGGAACTGATCAGCCGTCTCTCAGACC	468
Oy	355	AACATGAGGGGCTGCTCTGATGATCTAGGAGGCTAAGGAACTGATCAGCCGTCTCTCAGACC	414
Db	469	AAAACACAGCCCCCATCGGTCTATCTACTGAGCCCTG	505
Oy	415	AAAAAGCACCCCACCCGCTCATCTACTGAGCCCTG	451
RESULT	14		
LOCUS	A13735	540 bp	DNA
DEFINITION	variable region of a monoclonal antibody which cross reacts with 19 known Pseudomonas aeruginosa serotypes.		
ACCESSION	A13735		
NID	g491743		
KEYWORDS	.		
SOURCE	unidentified.		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 540)		
AUTHORS	Domdey,H., Marget,M. and von Specht,B.U.		
TITLE	Monoclonal antibodies to Pseudomonas aeruginosa, their production and use		
JOURNAL	Patent: EP 038395-A 3 25-OCT-1989;		
FEATURES	BEHRINGWERKE Aktiengesellschaft		
Source	Location/Qualifiers		
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CDS	/organism="Artificial sequences"		
	64..>540		
	/product="V region monoclonal antibody,cross reacts with 19 known P.aeruginosa serotypes"		
	/db_xref="PID:g491744"		
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BASE COUNT	145 a 144 c 130 g 121 t		
ORIGIN			
Query Match	59.7%; Score 275; DB 22; Length 540;		
Best Local Similarity	83.4%; Pied.No.1,54e-185;		
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Oy	1 ATGGAATCAGACTGGGTCTTTCTCTCTCTGTCATTAATACAGAGTGCACATCCAG	60	
Db	124 GTTCCAGCTTACAGACTGTGGGGCTGAATGGCAAACCTGGGGCTCATGTAGAATGTCC	183	
Oy	61 GCTATTCTTACAGACAGTCTGGGGCTGAGCTGGTAGAGTCTGGGGCTCATGTAGAATGTCC	120	

 (TM)

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MParch_n n.a. - n.a. database search, using Smith-Waterman algorithm
 P on: Sat Apr 17 15:48:10 1999; MasPar time 71.03 Seconds
 883.040 Million cell updates/sec
 Par output not generated.

Title: >US-08-836-455-3
 Description: (1-461) from US08836455.seq
 Perfect Score: 461
 N.A. Sequence: 1 ATGGATGACGCTGGCTTT.....CTGGCTCCCTGGAGCTTGGG 461
 Comp: TACCTTACGCTGCACCCAGAA.....GACCAGGACCTTCGAAACC

Scoring table: TABLE default
 Gap 6

Mmatch STD : Dbase 0; Query 0

Searched: 188442 seqs, 68026449 bases x 2

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database:

n-geneseq32
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
 14:part14 15:part15 16:part16 17:part17 18:part18
 19:part19 20:part20 21:part21 22:part22 23:part23
 24:part24 25:part25 26:part26 27:part27 28:part28
 29:part29 30:part30 31:part31 32:part32 33:part33
 34:part34 35:part35 36:part36 37:part37 38:part38
 39:part39 40:part40

Stats: Mean 8.375; Variance 5.103; scale 1.641

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	461	100.0	461	34	Murine monoclonal ant	1.66e-296
2	314	68.1	458	1	2H7 Vh sequence.	7.28e-194
3	314	68.1	491	39	Mouse 2H7 antibody he	7.28e-194
4	314	68.1	491	40	Mouse 2H7 antibody he	7.28e-194
5	314	68.1	491	40	Mouse 2H7 antibody he	7.28e-194
6	314	68.1	491	31	Mouse 2H7 antibody he	7.28e-194
7	314	68.1	518	32	2H7 heavy chain varia	7.28e-194
8	314	68.1	520	30	2H7 antibody heavy ch	7.28e-194
9	306	66.4	453	2	Coding sequence for h	2.64e-188
10	279	60.5	1570	2	2H7 Vh sequence which	1.42e-188
11	275	59.7	540	1	Monoclonal antibody O	8.39e-167
12	274	59.4	1395	30	Heavy chain of monoc	4.13e-166
13	274	59.4	1395	30	3F4 (chimeric) human	4.13e-166
					Murine anti-porcine V	4.13e-166

14	274	59.4	3400	30	T62937	3F4 human G2/G4 chime	4.13e-166
15	274	59.4	5300	30	T62938	3F4 human IgG4 expres	4.13e-166
16	273	59.2	358	7	043385	H-chain V-region of m	2.04e-165
17	266	57.7	408	11	066846	Sequence encoding the	1.43e-160
18	265	57.5	1581	8	048037	Monoclonal antibody M	7.01e-160
19	263	57.0	420	11	065631	Murine variable regio	1.70e-158
20	263	57.0	690	33	T85090	Mouse monoclonal anti	1.70e-158
21	263	57.0	9208	11	065629	Vector contg. TCAE 8	1.70e-158
22	261	56.6	411	24	T35051	Mab VLI7E6 heavy chai	4.10e-157
23	259	56.2	10844	7	043848	Plasmid PAH4808.	9.90e-156
24	258	56.0	450	1	004695	Heavy chain variable	4.86e-155
25	257	55.7	10704	7	043846	Plasmid PAH4625.	2.39e-154
26	257	55.7	11529	7	043844	Plasmid PAH602.	2.39e-154
27	255	55.3	417	7	043843	Chimeric 128.1 Vh, mo	5.76e-153
28	255	55.3	458	3	015164	Vh186 region of anti-	5.76e-153
29	253	54.9	499	29	T38509	Heavy chain coding se	1.39e-151
30	253	54.9	1553	14	079930	Anti-tobacco mosaic v	1.39e-151
31	252	54.7	443	1	N91820	DNA sequence of the V	6.81e-151
32	252	54.7	12132	7	043847	Plasmid PAH807.	6.81e-151
33	249	54.0	453	7	043593	Sequence encoding mur	8.03e-149
34	248	53.8	416	34	T85854	Anti-HMFG Mab CTMO1 h	3.94e-148
35	248	53.8	420	1	N90671	DNA sequence encoding	3.94e-148
36	248	53.8	474	3	020380	Sequence of Vhinge ge	3.94e-148
37	247	53.6	417	39	V01097	Heavy chain variable	1.93e-147
38	247	53.6	417	5	030758	p64-12.	1.93e-147
39	247	53.6	1773	38	T88869	H chain subunit of Fa	1.93e-147
40	246	53.4	416	6	038877	CTMO1 Vh cDNA.	9.46e-147
41	244	52.9	399	16	090425	DNA encoding anti-idi	2.27e-145
42	244	52.9	402	16	090426	DNA encoding anti-idi	2.27e-145
43	244	52.9	468	2	012062	Sequence encoding mou	2.27e-145
44	244	52.9	468	2	012018	Sequence encoding mou	2.27e-145
45	243	52.7	450	7	043596	Sequence encoding mur	1.11e-144

ALIGNMENTS

RESULT 1
 ID T85150 standard; cDNA: 461 BP.
 AC T85150;
 DT 04-JAN-1998 (first entry)
 DE Murine monoclonal anti-idiotype antibody 11D10 Vh cDNA.
 KW Monoclonal antibody 11D10: anti-idiotype antibody; mucin;
 KM human milk fat globule; HMFG; tumour; breast cancer; vaccine; ss.
 OS Mus musculus.
 FH Key
 FT sig_peptide Location/Qualifiers
 FT 1..57 /tag= a
 FT mat_peptide 58..461
 FT /tag= b
 PN WO9722699-A2.
 PD 26-JUN-1997.
 PF 19-DEC-1996; U20757.
 PR 13-DEC-1996; US-575762.
 PR 20-DEC-1995; US-575762.
 PR 26-JAN-1996; US-591965.
 PI (KENT) UNIV KENTUCKY.
 PA Chatterjee M, Chatterjee SK, Foon KA;
 DR WPI: 97-341690/31.
 DR P-PSDB: W27120.
 PT Monoclonal anti-idiotype antibody 11D10 - elicits immune response
 PT against human milk fat globule disease associated tumours,
 PT especially breast cancer
 PS Claim 12: Page 94; 130pp; English.
 CC This cDNA sequence encodes the heavy chain variable region Vh
 CC (W85150) of monoclonal anti-idiotype antibody 11D10 produced by
 CC hybridoma cell line ATCC 12020. 11D10 was obtained by immunising
 CC naive mice with WC-10 anti-HMFG antibody to obtain an anti-idiotype
 CC response. It elicits an immune response against a specific epitope
 CC of a high mol.wt. mucin of human milk fat globule (HMFG). It
 CC induces an immunological response to HMFG in mice, rabbits, monkeys
 CC and patients with advanced HMFG-associated tumours. Pharmaceutical
 CC compositions and vaccines comprising 11D10, 11D10 polypeptides
 CC and/or 11D10 polynucleotides are claimed. Also claimed are

Query Match	100.0%	Score 461;	DB 34;	Length 461;
Best Local Similarity 100.0%;	Prod. No. 1,66e-256;			
Matches 461; Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
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Qy	1	ATGGAATGCAGCTGGGTCTTCTCTCTCTCTCTCTGCAATTAAGGTGTCCACTCCAG	60	
Db	61	gcttatctacagcagctctgagctgagctggtgagctctggtggtcctcagtgagatgtcc	120	
Qy	61	GCTTATCTACAGCAGCTGGGGCTGAGCTGTGAGGTGTGGGGCTCAGTGAAGATGTCC	120	
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Qy	181	GGACAGGCGCTTGGATGGATTTGAAATTTTCTCTGGAATGGTGAATCTTACTTACAAT	240	
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Qy	301	CAGATCAGCAGCCTCTGACATCTGAAGAGACTCTGGCTTATTTCTGTGCAAGAGGAACCTGG	360	
Db	361	gagggtgctctgagcactctggtggtcaaggaaacctacacgctctccttaagccaagaag	420	
Qy	361	GAGGTGCTCTGAGCTACTGTGGGTCAAGGAACCTCAGTCACCGTCTCTCTCAGCCAAAAG	420	
Db	421	acacccccacccgctctatccactgtcccttgaagaacttgg	461	
Qy	421	ACACCCCCACCCGCTCTATCCACTGTCCCTTGAAGCTTTGG	461	
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ID	N91146	standard; DNA; 458 BP.		
AC	N91146;			
DT	06-JUL-1990	(first entry)		
DT	2H7 VH sequence.			
CD	Antibodies; passive immunisation; pH3-6a; ss.			
OR	Synthetic.			
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FT	misc_feature	398..408		
FT		/*tag- b		
FT	misc_feature	/note="Sequence homologous to DSP.2"		
FT		360..406		
FT		/*tag- c		
FT		/note="JH1 region"		
DR	NO8900999-A.			
PT	9-FEB-1989.			
PT	25-JUL-1988; 02514.			
PR	24-JUL-1987; US-077528.			
PA	(ITGE-) Int Genetic Eng Inc.			
PR	Robinson RR, Liu AY, Horwitz AH, Wall R, Better M;			
DR	WHL; 89-061144/08.			
PT	P-PSDB; P94780.			
PT	Polynucleotide(s) encoding immunoglobulin molecules -			
PT	used for efficient prodn. of chimeric human or non-human or			
PT	class switched antibodies.			
PS	Sequence carries 2H7 VH region of the chimeric immunoglobulin sequence.			
CC	The antibodies are useful in passive immunisation avoiding negative			
CC	immune reactions. They are also useful in assaying and in vitro imaging			

SQ	Sequence	458 BP;	113 A;	120 C;	112 G;	113 T;
	Query Match	68.1%;	Score 314;	DB 1;	Length 458;	
	Best Local Similarity	94.6%;	Pred. No. 7,28e-194;			
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					0;	Gaps
						0.
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Oy	1 ATGGAATGCAGCTGGGCTTCTTCCTCCTCGTCAATAACTACAGGTGCCACTCCAG	60				
Db	99 gctattccaacgacgctcggggacctggtgtgagcgctcggggacctgaftgaagtcc	158				
Oy	61 GCTATTCTACAGCAGCTCGGGGCTGAGCTGGTGAGGCTCGGGGCTCATGTAATATSTCC	120				
Db	159 tcgaaggttttgctctaccatactaccagttacaatatgcactggtftraagaacaaacct	218				
Oy	121 TGCANAGCTTTGGCTACACTTACACAGTTACAAATATGCACTGGTGAAGCAACACCT	180				
Db	219 agacagggccctggaatgatgttgagcatattatcccaagaaatgltgtaactctacaat	278				
Oy	181 GGACAGGGCCCTGGAATGATTTGGAATAATTTTCTCTGGAATATGTTACTACTACAAT	240				
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Oy	241 CAGAAGTTTAAGGGCCAAGGGCCTCATTTGACTGCAACACATCTCTCCACACAGCCTACATG	300				
Db	339 cagctcagaacacctgacactcgtgaagatctggsgtctattcttgtgaagag	390				
Oy	301 CAGATCACACACCCTGACATCTGAAGACTCTGGCTATTCTTGTSCAAGAG	352				
RESULT	3					
ID	V18557	standard; cdNA; 491 BP.				
AC	V18557;					
DE	05-JUN-1998	(first entry)				
DE	Mouse 2H7 antibody heavy chain variable region cDNA.					
KW	Mouse; murine; heavy chain; variable region;					
KW	immunoglobulin fragment production; Ig fragment production;					
KW	monoclonal antibody 2H7; human B-cell surface antigen; ss.					
OS	Mus sp.					
FH	Key	Location/Qualifiers				
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FT		/*tag= a				
FT	mat_peptide	129..491				
FT		/*tag= b				
FN	US5698435-A.					
ED	16-DEC-1997.					
PF	06-JUN-1995;	467140.				
PR	29-MAR-1990;	US-501092.				
PR	01-NOV-1985;	US-793980.				
PR	27-OCT-1986;	WO-003269.				
PR	24-JUL-1987;	US-077528.				
PR	11-JAN-1988;	US-142039.				
PR	08-DEC-1992;	US-987555.				
PR	18-AUG-1994;	US-299085.				
PR	06-JUN-1995;	US-467140.				
PA	(XOMA) XOMA CORP.					
P1	Better M, Horwitz AH, Lei S, Liu AY, Robinson RM.	*				
P1	Wall R, Wilcox GL;					
DR	WPJ; 98-051492/05.					
DR	P-PDSB; W47513.					
PT	DNA encoding secretable immunoglobulin fragments - comprising at					
PT	least the variable regions of light or heavy chains					
PS	Example IV; Fig 21; 98pp; English.					
CC	The present sequence was used in the development of a novel method					
CC	for the production of an immunoglobulin (Ig) fragment capable of					
CC	binding an antigen. The method comprises culturing an E. coli host					
CC	cell has been transformed with a nucleic acid molecule encoding the					
CC	Ig fragment, under conditions so that the Ig fragment is produced					
CC	and secreted. The nucleic acid molecule comprises DNA sequences					
CC	encoding: (a) pectate lyase secretion signal sequence operably					
CC	linked to a DNA sequence encoding at least the variable region of					
CC	an Ig Fd molecule; and (b) pectate lyase secretion signal sequence					


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FT mat_peptide 129..491
FT /tag= b
PN US5698417-A.
PF 16-DEC-1997.
PR 06-JUN-1995; 466203.
PR 29-MAR-1990; US-501092.
PR 01-NOV-1985; US-793980.
PR 27-OCT-1986; WO-002269.
PR 24-JUL-1987; US-077528.
PR 11-JAN-1988; US-142039.
PR 08-DEC-1992; US-987555.
PR 18-AUG-1994; US-299085.
PR 25-MAY-1995; US-450731.
PR 06-JUN-1995; US-466203.
PA (XOMA ) XOMA CORP.
PI Better M, Horwitz AH, Lei S, Liu AY, Robinson RR,
PI Wall R, Wilcox GL.
PI WPI; 98-051487/05.
DR P-PsDB; W47520.
DE Production of recombinant immunoglobulin fragment - comprising Fd
DE molecule and light chain
DE Example IV; Fig 21; 98pp: English.
CC The present sequence was used in the development of a novel method
CC for the production of an immunoglobulin (Ig) fragment capable of
CC binding an antigen. The method comprises culturing an E. coli host
CC that has been transformed with a nucleic acid molecule encoding the
CC Ig fragment, under conditions so that the Ig fragment is produced
CC and secreted. The nucleic acid molecule comprises DNA sequences
CC encoding: (a) pectate lyase secretion signal sequence operably
CC linked to a DNA sequence encoding at least the variable region of
CC an Ig Fd molecule; and (b) pectate lyase secretion signal sequence
CC operably linked to a DNA sequence encoding at least the variable
CC region of an Ig light chain, where (a) and (b) are operably linked
CC to a single prokaryotic promoter to form a dicistronic
CC transcription unit. The method is used to produce chimeric Fab
CC molecules, e.g. derived from murine monoclonal antibody 2H7 raised
CC against human B-cell surface antigen. The invention provides a
CC novel approach for producing genetically engineered antibodies of
CC desired variable region specificity and constant region
CC properties. The cloned Ig gene products can be produced by
CC expression in genetically engineered organisms. The application of
CC chemical gene synthesis, recombinant DNA cloning and production of
CC specific Ig chains in various organisms provides an effective
CC solution for the efficient large scale production of human
CC monoclonal antibodies. The invention also provides a solution to
CC the problem of class switching antibody molecules.
CC Sequence 491 BP; 113 A; 152 C; 113 G; 113 T;
SQ
Query Match 68.1%; Score 314; DB 40; Length 491;
Best Local Similarity 94.6%; Pred. No. 7,28e-194;
Matches 333; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
Db 72 atggagttcagcagatcttctctctctcctcgtcagtaactacagtggtccactccag 131
QY 1 ATGGAATGACGCTGGGCTCTTCTCTCTCTCTCTCTCAATACATACAGGTCTCCACGTC 60
Db 133 gttattctacacagctctggtggtcgtgagcgtgagggcctggggcctcagtgagatgtcc 191
QY 61 GCTTATCTACACAGCTGCTGGGCTGAGCTGTGAGGTCTGGGGCTCAATGAGAGTCTCC 120
Db 192 tgcaggctctcgtgtacacatttaccagttacaatatcactggtgtaagaagacact 251
QY 121 TCCAGAGCTTCTGGCTACACATTGACCAATTCATATCCTACTGGTTAAGCAGACACT 180
Db 252 agacagggccttggaatgagttgagactttatccaggaagtgtgatacttgtaacaat 311
QY 181 GGACAGGGCTCGAATGATGGAATATTTTCTCGGAATGGTATATCTACTACATCAAT 240
Db 312 cagaagttcagaagcagaagccactgactgtagacaatcctccagcagcactacatg 371
QY 241 CAGAAGTTTAAAGGAGGCTTCATTCATTCAGACACACTCTCCAGCAGACGCTCATG 300
Db 372 cagtcacagcagcctgacatctgaagactgtggtctattctgtgcaag 423

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QY 301 CAGATCAGCAGCCTGACATCTGAAGACTCTGGGCTCTATTCTGTGCAAGAG 352
|||||
RESULT 6
ID T70868 standard; cDNA; 491 BP.
AC T70868;
DT 04-SEP-1997 (first entry)
DE 2H7 heavy chain variable sequence.
KW Antibody engineering; heavy chain; light chain; chimeric antibody;
KW passive immunisation; diagnosis; hybridoma; monoclonal antibody;
KW 2H7; B-cell antigen; Bp35; ss.
OS Mus sp.
PH Key
FH signal_peptide 72..128
FT /tag= a
FT mat_peptide 129..491
FT /tag= b
FT misc_feature 393..439
FT /tag= c
FT /note= "JH1 sequence element"
FT misc_feature 429..439
FT /tag= d
FT primer_bind 469..490
FT /note= "DSP.2 sequence element"
FT /tag= e
FT /note= "primer JHBSEIT"
PN US5618920-A.
PD 08-APR-1997.
PE 01-NOV-1985; 793980.
PR 01-NOV-1985; US-793980.
PR 27-OCT-1986; WO-002269.
PR 24-JUL-1987; US-077528.
PR 11-JAN-1988; US-142039.
PR 29-MAR-1990; US-501092.
PR 17-APR-1992; US-870404.
PR 29-APR-1994; US-235225.
PA (XOMA ) XOMA CORP.
PI Better M, Horwitz AH, Lei S, Liu AY, Robinson RR;
PI Wall R, Wilcox GL;
PI WPI; 97-225473/20.
DR P-PsDB; W16343.
DE Secretible immunoglobulin heavy and light chain fragments - capable
DE of assembling into chimeric antibodies, useful for e.g. passive
DE immunisation, diagnosis, etc
DE Example 4; Fig 21; 96pp: English.
DE A cDNA clone (T70868) codes for the heavy chain variable region
DE (W16343) of the 2H7 mouse monoclonal antibody, which recognises
DE human B-cell surface antigen Bp35. The sequence was isolated from
DE a 2H7 cell line cDNA library by PCR amplification. The 2H7 light
DE chain variable sequence (760869) has also been isolated. The
DE sequences have been used to construct a human-mouse chimeric
DE antibody with specificity for the human B-cell antigen.
DE Sequence 491 BP; 113 A; 153 C; 112 G; 113 T;
SQ
Query Match 68.1%; Score 314; DB 31; Length 491;
Best Local Similarity 94.6%; Pred. No. 7,28e-194;
Matches 333; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
Db 72 atggagttcagcagatcttctctctcctcgtcagtaactacagtggtccactccag 131
QY 1 ATGGAATGACGCTGGGCTCTTCTCTCTCTCTCTCTCAATACATACAGGTCTCCACGTC 60
Db 132 gttattctacacagctctggtggtcgtgagcgtgagggcctcagtgagatgtcc 191
QY 61 GCTTATCTACACAGCTGCTGGGCTGAGCTGTGAGGTCTGGGGCTCAATGAGAGTCTCC 120
Db 192 tgcaggctctcgtgtacacatttaccagttacaatatcactggtgtaagaagacact 251
QY 121 TCCAGAGCTTCTGGCTACACATTGACCAATTCATATCCTACTGGTTAAGCAGACACT 180
Db 252 agacagggccttggaatgagttgagactttatccaggaagtgtgatacttgtaacaat 311

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Qy	181	GCACGAGGGCCCTGGAATGGATTGGAAATATTTTTCCTGGAAAATGCTATTAATTACTAAT	240
Db	312	cagaagttcaagggaagccacactgactgtagacaatacctccagcagcctacatg	371
Qy	241	CAGAACTTTAAAGGGCAAGCCCATTTGACTCGAGACACATCTCTCCAGCAGCCTACATG	300
Db	372	cagctcagcagcctgacatctgaagactctgggtctatcttctgtgcaagag	423
Qy	301	CAGATCAGCAGCAGCCTGACATCTGAAACACTCTGGGCTATTTCTGTGCAAGAG	352
RESULT 7			
ID	T36316	standard; cDNA; 518 BP.	
AC	T36316;		
DT	21-OCT-1997	(first entry)	
DE	2H7 antibody heavy chain variable region cDNA.		
KW	Immunoglobulin G; IgG; heavy chain; recombinant production; antibody; passive immunisation; serum sickness; anaphylactic shock; immunosassy; imaging; reagent; complement mediated lysis; therapy; variable region; ss.		
MM	Mus spp.		
Key	Location/Qualifiers		
FT	signal_peptide	71..127	
FT	mat_peptide	/*tag- a 128..490	
FT	mat_peptide	/*tag- b	
PN	US5595898-A.		
PF	21-JAN-1997.		
PD	01-NOV-1985; 793980.		
PR	29-MAR-1980; US-501092.		
PR	01-NOV-1985; US-793980.		
PR	27-OCT-1986; WO-002269.		
PR	24-JUL-1987; US-077528.		
PR	11-JAN-1988; US-142039.		
PR	08-DEC-1992; US-987555.		
PR	18-AUG-1994; US-299085.		
PA	(XOMA) XOMA CORP.		
PI	Better M, Horwitz AH, Lei S, Liu AY, Robinson RR;		
PI	Wall R, Wilcox GL;		
DR	WPI: 97-107579/10.		
DR	P-PSDB; W10588.		
PT	Nucleic acid encoding immunoglobulin fragment - comprising		
PT	electronic transcription unit with pectate lyase signal sequences		
PS	Example; Fig 21; 95pp; English.		
CC	The present sequence encodes the heavy chain variable region of		
CC	the 2H7 antibody. The 2H7 cDNA was used in the preparation of		
CC	a novel polynucleotide molecule encoding an Ig fragment. The DNA		
CC	molecule comprises 2 DNA sequences encoding 2 pectate lyase		
CC	secretion signal sequences respectively linked to a DNA sequence		
CC	encoding an Ig Fd molecule or Ig light chain, operably linked to a		
CC	single prokaryotic promoter so as to form a dicistronic		
CC	transcription unit, provided that the Ig fragment can bind an		
CC	antigen and is produced and secreted by an E. coli host cell when		
CC	the nucleic acid molecule is expressed in the host cell.		
CC	The polynucleotide molecule is used for the production of		
CC	recombinant antibodies, which can be used for passive immunisation		
CC	without negative immune reactions (e.g. serum sickness and		
CC	anaphylactic shock), in labelled forms as immunoassy or imaging		
CC	reagents, in complement mediated lysis and for therapeutic		
CC	purposes when coupled to a toxin or other therapeutic agent.		
CC	Sequence 518 BP; 113 A; 152 C; 140 G; 113 T;		
SO			
Query Match 68.1%; Score 314; DB 32; Length 518;			
Best Local Similarity 94.6%; Pred. No. 7,28e-194;			
Matches 333; Conservative 0; Mismatches 19; Indels 0; Gaps 0			
Db	71	atgaggtatcagcagagatcttctcttccctctgtaactacagtggtccactccag	130
Qy	1	ATGAATGACAGCTGGGCTGCTTCTCTCTCTCTCTCTGTAATAACTACAGGTGCTACCTCCAG	60
Db	131	gcttatctacagcagctctggggctgtagctgtgttagagcctcgggctcagtgaaagtcc	190
Qy	61	GCTATCTACACAGCACTCTGGGGCTAGCTGTGAGAGTCTGGGGCTCTGTAAGATGTC	120

Dd	191	tgcagggcttctggtacacattccaggttacaatalgcactgggtaaagaacacct	250
Oy	121		
Oy	121	tcacaggccttccgtccatcacattgccaggttacatattgacctgggttaaacgacacct	180
Dd	251	aacagggcgcttgaaatgatggagtcttatccaggaatatggtacttccacaat	310
Oy	181		
Oy	181	ggacagggcgcttgaaatggaaattgaaaatttttcttggaaaatngtgatacttactacat	240
Dd	311	cagaagttcaaggcgaagcccacactgactctgagacaatatcctccagcacgccccatg	370
Oy	241	cagaaagtttaagggcgaagccctcatctgacatgcagacacatctccagcacagccctacatg	300
Dd	371	caagctcagcagccttgacatctgaagaactctgcygtctattcttgtcaagag	422
Oy	301		
Oy	301	cagatcagcagccttgcacatctgamaacactctgcgctctatttctgtgcaagag	352
<hr/>			
RESULT 8			
ID	TS1042 standard; cDNA; 520 BP.		
AC	TS1042:		
Dd	06-AUG-1997 (first entry)		
DE	Coding sequence for heavy chain variable region of 2H7.		
KM	Pectate lyase; signal sequence; Gram-negative bacterium; immunoglobulin;		
KM	protein production; human; constant region; passive immunisation; toxin;		
KM	serum sickness; anaphylaxis; sweetener; thumatin; cytoplasm; periplasm;		
KM	antibody; Ig; heavy-chain; hepatitis; mouse; lung carcinoma; cancer;		
OS	Mus musculus.		
FH	Key	Location/Qualifiers	
FT	cds	71..490	
FT		/tag= a	
FT		/product= heavy chain variable region of 2H7	
FN		/note= "no stop codon given"	
PD	US5576195-A.		
PE	19-NOV-1996.		
PR	01-NOV-1985; 793980.		
PR	01-NOV-1985; US-793980.		
PR	27-OCT-1986; WO-002269.		
PR	24-JUL-1987; US-077528.		
PR	11-JAN-1988; US-142039.		
PR	29-MAR-1990; US-501092.		
PR	08-DEC-1992; US-987555.		
PR	22-FEB-1993; US-020671.		
PR	09-DEC-1994; US-357234.		
PA	(XOMA) XOMA CORP.		
PI	Better M., Lei S., Robinson RR, Wilcox GL;		
DR	WPI: 97-011254/01.		
DR	P-PsDB: W12042.		
PT	Improved prodn. of protein in Gram -ve bacteria using signal		
PT	sequence - from pectate lyase to ensure transport of protein from		
PS	the cytoplasm, esp. for prodn. of antibodies		
PS	Example 4; Fig 21; 86pp: English.		
CC	This sequence represents the coding sequence for the heavy chain variable		
CC	region of the 2H7 mouse monoclonal antibody. The 2H7 antibody recognises		
CC	the human B-cell surface antigen Bp35, which plays a role in B-cell		
CC	activation. This sequence was used in a human-mouse chimeric antibody		
CC	with human B-cell antigen specificity, that was produced using the method		
CC	of the invention. The method of the invention is for the production of a		
CC	protein in a Gram-negative bacterium. The method improves on current		
CC	techniques, by using a vector including DNA encoding the pectate lyase		
CC	signal sequence (see T51034), attached to the sequence encoding the		
CC	protein for production. The method is especially used to make		
CC	immunoglobulins (Ig), particularly those with a human constant region,		
CC	suitable for passive immunisation (without risk of serum sickness or		
CC	anaphylaxis) or for in vivo/in vitro diagnosis and imaging. The Ig may		
CC	also be used therapeutically, optionally coupled to toxins, etc.		
CC	Alternatively the protein to be produced is the sweetener thaumatococcus.		
CC	The presence of this signal sequence means that the protein is exported from		
CC	the cytoplasm and can be recovered from the culture medium or periplasm,		
CC	in active and correctly folded form. The method allows the class of any		
CC	reduced and acid-stable, and these can now be changed to G, A or F		
CC	and/or to be switched, e.g. most human-human Ig are of m class, easily		

ID	NT0971	standard	CDNA: 459 BP.
DT	NT0971;		
DE	09-APR-1991	(first entry)	
DE	217	VH sequence which contains JH1 sequences and DSP.2 sequence elements.	
DE	Chimeric antibody; Anti-cancer antibody; ss.		
FM	key	Location/Qualifiers	
FT	cds	39..95	
FT		/*tag= a	
FT		/label=leader peptide	
FT	cds	96..185	
FT		/*tag= b	
FT		/label=FR1	
FT	cds	186..200	
FT		/*tag= c	
FT		/label=CDR1	
FT	cds	201..242	
FT		/*tag= d	
FT		/label=FR2	
FT	cds	245..293	
FT		/*tag= e	
FT		/label=CDR2	
FT	cds	294..389	
FT		/*tag= f	
FT		/label=FR3	
FT	cds	390..428	
FT		/*tag= g	
FT		/label=CDR3	
FT	cds	429..459	
FT		/*tag= h	
FT		/label=FR4	
FT	cds	411..459	
FT		/*tag= i	
FT		/label=JH1	
PN	W08702671-A.		
PD	07-MAY-1987.		
PF	27-OCT-1986;	U02269.	
PR	01-NOV-1985;	US-793980.	
PA	(ITGE-) INT GENETIC ENG INC.		
PA	(ROBI) ROBINSON R R.		

Query Match	Score	DB	Length
56.4%	306	DR	459
Best Local Similarity	94.1%	Pred. No. 2,646-188	
Matches	332	Conservative	0; Mismatches 20; Indels 1; Gaps 1
Db	39	atggattcagcagagatctctctcctcctgcagtaactaagaqgttcactcca	98
Qy	1	ATGGAAATCAGACTGGGCTTTCTCTTCTCTCTCTGTCATTAATACAA-GGTGTCCACTCCCA	59
Db	99	ggctatctacagcagcagcttggggcttgagcttggtgagggccttcagtgaaatgctc	158
Qy	60	GCGTATATACAGCAGCTGTGGGCTGAGCTGGTGAAGCTGTGGGCTCAGTGAAGATGTC	119
Db	159	ctgcgaagctctctggtctacacatttaccagttacaatatgacgcgggttaagcagaacc	218
Qy	120	CTGCAGAGCTTCTGGCTACACATTGACAGTAATCAATAATGCACGGGTAAAGCAGACACC	179
Db	219	tagaagaagccttggaatgagcttgagcattatccagaagaatggtatctctacaa	278
Qy	180	TGGACAGGGCCTCGAATGATTTGAAATATTTTCTCTGGAATGCTGACTTACTCTCAA	239
Db	279	tcaagaagtcgaagggcaagggccacacactgagctgtagacaatccctccagcagcctacat	338
Qy	240	TCAGAGATTGAAGGCAAGCCCTATTGACGACAGACACATCCCTCCAGCAGCCTACAT	299
Db	339	gcagctcagcgcctgacatctgaagactctgcgtctattctgtgcaagag	391
Qy	300	GCAGATCAGAGCCTGACATCTGAAGACTCGCGTCTATTTCTGTGCAAGAG	352
RESULT	10		
ID	Q12637	standard; DNA; 1570 BP.	
AC	Q12637		
DE	03-OCT-1991	(first entry)	
DR	Monoclonal antibody OK3T	heavy chain coding sequence.	
KW	OK3T; heavy chain; humanised antibodies; CDR-grafting; ss.		
OS	Mus musculus.		
FH	Key	Location/Qualifiers	
FT	signal_peptide	41..97	
FT		/*tag= a	
FT	mat_peptide	98..1447	
FT		/*tag= b	
FT		/product= OK3T heavy chain	
PN	WO9109967-A.		
PN	WO9109968-A.		
PD	11-JUL-1991.		
PF	21-DEC-1990.		
PR	21-DEC-1989; GB-028874.		
PR	21-DEC-1990; WO-602017.		
PA	(CELL-) CELITECH LTD.		
PI	Adair JR, Athwal DS, Emtage JS;		
DR	WPI: 91-222915/30.		
DR	P-PsDB: R13061.		
PT	New humanised antibodies comprising CDR grafted antibody - with heavy and light chains, for use in in vivo therapy and diagnosis		

Matches 365; Conservative 0; Mismatches 79; Indels 2; Gaps 2;

Db 1 atgaagtgaagctgggtattctctccctccctcgaactcgcggcgctccacg 60
1 ATGAAGTGAAGCTGGGTATTCTCTCCCTCCCTCAATACTACAGGTCTCCATCCAG 60
61 gtccaagtcacagcctgggtggtggtggtggtggtggtggtggtggtggtggtc 120
61 GCTTACTACACAGCTGTGGGTGAGCTGTGAGCTGTGGGTGAGCTGTGGGTGAGCTGTG 120
121 tgcgaagctctgtgtacaaatttaagtaagtaagtaagtaagtaagtaagtaagta 180
121 TGCAGAGCTCTGTGTACAAATTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 180
181 ggaagagctgtgaatggtggtggtggtggtggtggtggtggtggtggtggtggt 240
181 GGACAGGCTGTGAATGATGAAATATTTTCTGGAATGATATTTCTTACTACAT 240
241 cagaagtcaggaggaagccacattgactgacagataaattccctcagcagcactacatg 300
241 CAGAAGTTAAGGCAAGGCTTATGACTGACAGACATCTCCACACAGGCTTACATG 300
301 caactcagcagcttgcacttgagactcgcgtctattactgtgcaagacgtacgta 360
301 CAGATCAGCAGCTGACATCTGAAAGCTGTGGGTCTATTGTGCAAGAGGGAAC-TG 359
361 ggaagctacttg-actactggggccaagggcaccacttcacagctcctcagcctcac 419
361 GGAGGCTGCTGTGACTACTGGGGTCAAGGACCTGACCTGCTCTCCACCAAAAC 419
420 caagggcccatccgcttcccccctgg 445
420 GACACCCCAACCCGCTATCCACTGG 445

RESULT 13
ID T62935 standard; DNA: 1395 BP.
AC T62935:
DE 16-JUN-1997 (first entry)
KW Murine anti-porcine VCAM 3F4 heavy chain DNA sequence.
KW Xenotransplantation; graft rejection; cell interaction; pig;
KW vascular cell adhesion molecule; VCAM; monoclonal antibody;
KW chimeric antibody; diagnosis; ss.
OS Mus sp.
PN MO9711971-A1.
PD 03-APR-1997; U15575.
PF 27-SEP-1996; U15575.
PI 28-SEP-1995; US-004489.
PI 26-SEP-1996; US-004489.
PI (ALEX-) ALEXION PHARM INC.
PI Evans MJ, Matlis LA, Mueller EE, Mueller JP, Rollins S;
PI Rother RP;
PI WPI: 97-212855/19.
PI P-PSDB: W14938.
PT Antibodies binding to porcine but not human cell interaction
PT proteins - useful to treat and assay for rejection of xenografted
PT porcine organs, tissues or cells
PS Disclosure: Page 53-55; 105pp; English.
CC DNA sequences (T62934-35) respectively code for the light chain
CC (W14937) and heavy chain (W14938) of murine anti-porcine soluble
CC vascular cell adhesion molecule (VCAM) monoclonal antibody (MAb)
CC 3F4. Hybridoma 3F4 was produced by standard techniques using
CC recombinant, soluble porcine VCAM as immunogen. Chimeric
CC antibodies can be produced by cloning MAb 3F4 and 2A2 (see also
CC T62929-30) variable regions into expression plasmid pAPEX-3p
CC modified to contain the human gamma4 constant region in place of
CC the human gamma1 C1 region. Sequences are provided for 3F4
CC (chimeric) human G2/G4 CDNA (T62936), a 3F4 human G2/G4 expression
CC plasmid insert (T62937), and a 3F4 human IgG4 expression plasmid
CC insert (T62938). The chimeric antibodies are specific for porcine
CC VCAM. They are useful for diagnosing human rejection of porcine
CC xenotransplants and for improving xenotransplantation of porcine
CC cells, tissues and organs into human recipients.

Sequence 1395 BP; 322 A; 429 C; 379 G; 265 T;

Query Match 59.4%; Score 274; DB 30; Length 1395;
Best Local Similarity 81.8%; Pred. No. 4.13e-166;
Matches 365; Conservative 0; Mismatches 79; Indels 2; Gaps 2;

Db 1 atgaagtgaagctgggtattctctccctccctcgaactcgcggcgctccacg 60
1 ATGAAGTGAAGCTGGGTATTCTCTCCCTCCCTCAATACTACAGGTCTCCATCCAG 60
61 gtccaagtcacagcctgggtggtggtggtggtggtggtggtggtggtggtggtc 120
61 GCTTACTACACAGCTGTGGGTGAGCTGTGAGCTGTGGGTGAGCTGTGGGTGAGCTGTG 120
121 tgcgaagctctgtgtacaaatttaagtaagtaagtaagtaagtaagtaagtaagta 180
121 TGCAGAGCTCTGTGTACAAATTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 180
181 ggaagagctgtgaatggtggtggtggtggtggtggtggtggtggtggtggtggt 240
181 GGACAGGCTGTGAATGATGAAATATTTTCTGGAATGATATTTCTTACTACAT 240
241 cagaagtcaggaggaagccacattgactgacagataaattccctcagcagcactacatg 300
241 CAGAAGTTAAGGCAAGGCTTATGACTGACAGACATCTCCACACAGGCTTACATG 300
301 caactcagcagcttgcacttgagactcgcgtctattactgtgcaagacgtacgta 360
301 CAGATCAGCAGCTGACATCTGAAAGCTGTGGGTCTATTGTGCAAGAGGGAAC-TG 359
361 ggaagctacttg-actactggggccaagggcaccacttcacagctcctcagcctcac 419
361 GGAGGCTGCTGTGACTACTGGGGTCAAGGACCTGACCTGCTCTCCACCAAAAC 419
420 caagggcccatccgcttcccccctgg 445
420 GACACCCCAACCCGCTATCCACTGG 445

RESULT 14
ID T62937 standard; DNA: 3400 BP.
AC T62937:
DE 16-JUN-1997 (first entry)
KW 3F4 human G2/G4 chimeric antibody expression plasmid insert.
KW Xenotransplantation; graft rejection; cell interaction; pig;
KW vascular cell adhesion molecule; VCAM; monoclonal antibody;
KW chimeric antibody; diagnosis; ss.
OS Chimeric Homo sapiens;
PN MO9711971-A1.
PD 03-APR-1997; U15575.
PF 27-SEP-1996; U15575.
PI 28-SEP-1995; US-004489.
PI exon
PI key
PI location/Qualifiers
PI 903..1055
PI /tag= a
PI /tag= a
PI /tag= 1056..1285
PI /tag= b
PI /tag= 1286..2055
PI /tag= c
PI /tag= c
PI /tag= 2056..2447
PI /tag= d
PI /tag= 2448..2483
PI /tag= e
PI /tag= 2484..2601
PI /tag= f
PI /tag= 2602..2928
PI /tag= g
PI /tag= 2929..3025
PI /tag= h
PI /tag= 3026..3348
PI /tag= i
PI /tag= 1

OY 241 CAGAGTTTAAAGGCAAGGCTCATTGACTGCAGACATCCTCCAGCAGACCTACATG 300
Db 1650 caactcaagcagcttggcactctgaagactctcgtctctattactgtgcaagacgtacgta 1709
OY 301 CAGATCAGCAGCCTGACACTGGAAGACTCTGCGGTCTATTCTGTGCAAGAGGAAC-TG 359
Db 1710 gaaagctacttg-actactggggccaaggcaccaactctcacagctctcctcagcctcac 1768
OY 360 GGAGGGTGTCTGTGACTACTGGGGTCAAGGAACCTCAGTCACCGTCTCTCTCAGCCAAAC 419
Db 1769 caaaggcccatccgctctcccccctgg 1794
OY 420 GACACCCCCACCCCGTCTATCCACTGG 445

Search completed: Sat Apr 17 15:51:42 1999
Job time : 212 secs.

MUSKIE (TM)

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Search - protein - protein database search, using Smith-Waterman algorithm
On: Thu Apr 15 18:00:56 1999; Maspar time 8.71 Seconds
657.976 Million cell updates/sec
Output not generated.

Title: >US-08-836-455-4
Description: (1-153) from US08836455.pep
Perfect Score: 1109
Sequence: 1 MECSWVFLFLSTITGVHSQ.....TVSSAKTTPPYPLVPGSL 153

Scoring table:
PAM 150
Gap 11

Searched: 116695 segs, 37453910 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: p1r58
1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 42.120; Variance 104.479; scale 0.403

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Hit	Score	Query Match	Length	ID	Description	Pred. No.
1	783	70.6	475	2	S01321	Ig gamma-2b chain pre 4.38e-106
2	780	70.3	474	2	S25057	Ig gamma-2b chain - m 1.38e-105
3	774	69.8	469	2	S37483	Ig gamma-2a chain - m 1.37e-104
4	767	69.2	151	2	PL0011	Ig heavy chain precu 2.00e-103
5	763	68.8	150	2	PN0444	Ig heavy chain V regi 9.21e-103
6	746	67.3	139	2	PS0024	Ig heavy chain precu 6.10e-100
7	742	66.9	166	2	PL0012	Ig heavy chain precu 2.81e-99
8	727	65.6	137	2	H32513	Ig heavy chain precu 8.57e-97
9	724	65.3	246	2	S38950	Ig gamma chain - mous 2.69e-96
10	724	65.3	446	2	S40295	Ig gamma-2a chain (ma 2.69e-96
11	710	64.0	178	2	S29584	Ig gamma chain (WMS5) 5.57e-94
12	709	63.9	140	1	HVMS67	Ig heavy chain precu 8.15e-94
13	708	63.8	138	2	S21810	Ig heavy chain V regi 1.19e-93
14	705	63.6	140	2	PH1482	Ig heavy chain V regi 3.74e-93
15	697	62.8	140	2	PH1489	Ig heavy chain V regi 7.84e-92
16	692	62.4	138	2	E32513	Ig heavy chain precu 5.25e-91
17	686	61.8	136	2	PL0208	Ig heavy chain V regi 5.13e-90
18	685	61.8	136	2	PL0208	Ig heavy chain precu 7.50e-90
19	684	61.7	141	2	A39276	Ig heavy chain precu 3.43e-89
20	681	61.4	140	2	PH1484	Ig heavy chain V regi 3.07e-88
21	678	61.1	139	2	A27609	Ig heavy chain precu 2.29e-88
22	676	61.0	135	2	A30577	Ig heavy chain precu 3.34e-88
23	675	60.9	135	2	PS0057	Ig heavy chain precu 3.34e-88

24	675	60.9	140	2	PH1498	Ig heavy chain V regi 3.34e-88
25	672	60.6	135	2 <th>PH1493</th> <th>Ig heavy chain V regi 1.04e-87</th>	PH1493	Ig heavy chain V regi 1.04e-87
26	671	60.5	137	2 <th>PH1227</th> <th>Ig heavy chain precu 1.53e-87</th>	PH1227	Ig heavy chain precu 1.53e-87
27	670	60.4	135	2 <th>PH1494</th> <th>Ig heavy chain V regi 2.23e-87</th>	PH1494	Ig heavy chain V regi 2.23e-87
28	670	60.4	135	2 <th>PH1492</th> <th>Ig heavy chain V regi 4.76e-87</th>	PH1492	Ig heavy chain V regi 4.76e-87
29	668	60.2	140	2 <th>PH1486</th> <th>Ig heavy chain V regi 2.17e-86</th>	PH1486	Ig heavy chain V regi 2.17e-86
30	664	59.9	140	2 <th>PH1483</th> <th>Ig heavy chain V regi 6.77e-86</th>	PH1483	Ig heavy chain V regi 6.77e-86
31	661	59.6	117	2 <th>S03289</th> <th>Ig heavy chain precu 6.77e-86</th>	S03289	Ig heavy chain precu 6.77e-86
32	661	59.6	133	2 <th>PC1155</th> <th>Ig heavy chain precu 6.77e-86</th>	PC1155	Ig heavy chain precu 6.77e-86
33	658	59.3	140	2 <th>A36194</th> <th>Ig heavy chain V regi 6.11e-85</th>	A36194	Ig heavy chain V regi 6.11e-85
34	655	59.1	139	1 <th>MHMS18</th> <th>Ig heavy chain precu 6.58e-85</th>	MHMS18	Ig heavy chain precu 6.58e-85
35	653	58.9	141	2 <th>FL0076</th> <th>Ig heavy chain precu 1.40e-84</th>	FL0076	Ig heavy chain precu 1.40e-84
36	651	58.7	137	2 <th>F29380</th> <th>Ig heavy chain precu 2.99e-84</th>	F29380	Ig heavy chain precu 2.99e-84
37	650	58.6	137	2 <th>E29380</th> <th>Ig heavy chain precu 4.37e-84</th>	E29380	Ig heavy chain precu 4.37e-84
38	645	58.2	117	1 <th>HVMSA1</th> <th>Ig heavy chain precu 2.90e-83</th>	HVMSA1	Ig heavy chain precu 2.90e-83
39	645	58.2	136	2 <th>S04576</th> <th>Ig heavy chain precu 2.90e-83</th>	S04576	Ig heavy chain precu 2.90e-83
40	642	57.9	131	2 <th>A27472</th> <th>Ig heavy chain precu 9.03e-83</th>	A27472	Ig heavy chain precu 9.03e-83
41	642	57.9	140	2 <th>S04575</th> <th>Ig heavy chain precu 9.03e-83</th>	S04575	Ig heavy chain precu 9.03e-83
42	637	57.4	136	2 <th>B47159</th> <th>Ig heavy chain V regi 5.98e-82</th>	B47159	Ig heavy chain V regi 5.98e-82
43	636	57.3	117	1 <th>HVMS8A</th> <th>Ig heavy chain precu 8.73e-82</th>	HVMS8A	Ig heavy chain precu 8.73e-82
44	635	57.3	137	1 <th>G2MS43</th> <th>Ig heavy chain precu 1.27e-81</th>	G2MS43	Ig heavy chain precu 1.27e-81
45	634	57.2	117	1 <th>HVMS3</th> <th>Ig heavy chain precu 1.86e-81</th>	HVMS3	Ig heavy chain precu 1.86e-81

ALIGNMENTS

RESULT 1
ENTRY S01321 #type complete
TITLE Ig gamma-2b chain precursor - mouse
ORGANISM #formal name Mus musculus #common name house mouse
DATE 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 08-Sep-1997

ACCESSIONS
REFERENCE S01320
#authors de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.;

#journal Eur. J. Biochem. (1988) 176:287-295
#title Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed against the tumour marker human placental alkaline phosphatase.

#cross-references M01D:88329081
#accession S01321
##molecule_type mRNA
##residues 1-475 ##label DEL
##cross-references EMBL:X13188; NID:951780; PID:951781
#note this sequence was determined from the differentiated gene

CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
KEYWORDS Immunoglobulin

FEATURE
1-19 #domain signal sequence #status predicted #label sig
20-475 #product Ig gamma-2b chain #status predicted #label MAT
159-223 #domain immunoglobulin homology #label IGG1

SUMMARY
#length 475 #molecular_weight 51567 #checksum 4120
Query Match 70.6%; Score 783; DB 2; Length 475;
Best Local Similarity 71.4%; Pred. No. 4.38e-106;
Matches 110; Conservative 22; Mismatches 18; Indels 4; Gaps 3;

DB	1	MEWIMFLITSTAGVQVQVQSGAELARRGASVKSCKRSGTTLNSYSGISWKRQT 60
OY	1	MECSWVFLFLSTITGVHSQVAYLQSGAELVRSKASGKSGTTLNSYNNHWWKQRP 60
DB	61	GQGLEWIGETIPGSGSYEFERKFKATLTVDSSTALVLSLSEDSAVYFCA-GPR 119
OY	61	GQGLEWIGETIPGSGSYEFERKFKATLTVDSSTALVLSLSEDSAVYFCA-RGM 120
DB	120	QVGLPFGYWGQGLTVASAKTTPPYPLAPG 153
OY	121	E-GAL--DWGQGSTVTSASAKTTPPYPLVPG 151

RESULT 2

ENTRY S25057 #type complete
TITLE Ig gamma-2b chain - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
ACCESSIONS S25057
REFERENCE S25057
#authors Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.V.; Kreuzaler, F.
#submission submitted to the EMBL Data Library, July 1992
#description Production of a Tobacco mosaic virus (TMV) inactivating neotop specific monoclonal antibody in Nicotiana tabacum.
#accession S25057
#status preliminary
#molecule_type mRNA
#residues 1-474 #label FIS
#cross-references EMBL:X67210; NID:954826; PID:954827
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
SUMMARY #length 474 #molecular-weight 52069 #checksum 4891
Query Match 70.3%; Score 780; DB 2; Length 474;
Best Local Similarity 71.1%; Pred. No. 1.38e-105;
Matches 108; Conservative 21; Mismatches 21; Indels 2; Gaps 2;
Db 1 MEMSWFLFLSGTAGHGEVLOQSGPELVNPGASVSKSCASGYFTITVYMHVQKRP 60
OY 1 MECSWFLFLSLTTTGVSQAAYLOQSGAELVRSASVSKSCASGYFTITVYMHVQKRP 60
Db 61 GGGLEWIGYINPNKDGITKEKEFKKATLTSDKSNATAYMELSLTSEDSAVYFCARD 120
OY 61 GGGLEWIGINIPGNGDTYNNQKFKKASLTADTSSSTAYMQLSLTSEDSAVYFCARG-N 119
Db 121 YD-WFAYWGQGLVYSAKTPPPVPLAPG 151
OY 120 WEGALDYWGQGSTVTVSSAKTTPPPVPLVPG 151
RESULT 3
ENTRY S37483 #type complete
TITLE Ig gamma-2a chain - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Sep-1997
ACCESSIONS S37483
REFERENCE S37483
#authors Duncanson, F.F.D.
#submission submitted to the EMBL Data Library, February 1993
#accession S37483
#status preliminary
#molecule_type mRNA
#residues 1-469 #label DUC
#cross-references EMBL:X70423; NID:940625; PID:9406253
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
KEYWORDS immunoglobulin
FEATURE 276-345
SUMMARY #domain immunoglobulin homology #label IG62
#length 469 #molecular-weight 51349 #checksum 7833
Query Match 69.8%; Score 774; DB 2; Length 469;
Best Local Similarity 72.5%; Pred. No. 1.37e-104;
Matches 108; Conservative 22; Mismatches 17; Indels 2; Gaps 1;
Db 4 SWIFLFLSGTAGVHCQILOQSGPELVNPGASVSKISCAAGTFTDYINWVQKPGOG 63
OY 4 SWVFLFLSLTTTGVSQAAYLOQSGAELVRSASVSKSCASGYFTITVYMHVQKPGOG 63
Db 64 LEMWIGYINPNKDGITKEKEFKKATLTVDSSSTAYMQLSLTSEDTAYVFCARANGATA 123
OY 64 LEMWIGITFPGNGDTYNNQKFKKASLTADTSSSTAYMQLSLTSEDSAVYFCAR--GNME 121
Db 124 TLLDYWGQGLTVSSAKTTPPPVPLAP 152
OY 122 GALDYWGQGSTVTVSSAKTTPPPVPLVP 150

RESULT 4
ENTRY PL0011 #type fragment
TITLE Ig heavy chain precursor V region (4C11) - mouse (fragment)
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 18-Oct-1996
ACCESSIONS PL0011
REFERENCE PL0011
#authors Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H.
#journal Mol. Immunol. (1998) 25:33-40
#title Structural basis of stimulatory anti-idiotypic antibodies.
#cross-references PubMed:88142863
#accession PL0011
#molecule_type mRNA
#residues 1-151 #label CHE
#experimental_source cell line 4C11
COMMENT This protein is an anti-idiotypic antibody that induces an anti-phosphorylcholine response.
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE 1-19
1-19 #domain signal sequence #status predicted #label SIG\
20-136 #product Ig heavy chain V region 4C11 #status predicted
50-54 #region complementarity-determining 1\
69-85 #region complementarity-determining 2\
118-125 #region complementarity-determining 3\
137-151 #domain C region (fragment) #status predicted #label COR
SUMMARY #length 151 #checksum 2479
Query Match 69.2%; Score 767; DB 2; Length 151;
Best Local Similarity 70.3%; Pred. No. 2.00e-103;
Matches 104; Conservative 22; Mismatches 21; Indels 1; Gaps 1;
Db 4 SWIFLFLSGTAGVSEVLOQSGPELVNPGASVSKISCAAGTFTDYINWVQKSHGS 63
OY 4 SWVFLFLSLTTTGVSQAAYLOQSGAELVRSASVSKSCASGYFTITVYMHVQKPGOG 63
Db 64 LEMWIGPNDNFENKFKPKATLTVDKSSSTAYMELSLTSEDSAVYFCASDY-GA 122
OY 64 LEMWIGNIPGNGDTYNNQKFKKASLTADTSSSTAYMQLSLTSEDSAVYFCARANGEGA 123
Db 123 IDYWGQGSTVTVSSAKTTPPPVPLAPG 150
OY 124 IDYWGQGSTVTVSSAKTTPPPVPLVPG 151
RESULT 5
ENTRY PN0444 #type fragment
TITLE Ig heavy chain V region precursor - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
ACCESSIONS PN0444
REFERENCE PN0444
#authors Kaluza, B.; Betz, G.; Shao, H.; Diamantstein, T.; Weidle, U.H.
#journal Gene (1992) 122:321-328
#title A general method for chimerization of monoclonal antibodies by inverse polymerase chain reaction which conserves authentic N-terminal sequences.
#accession PN0444
#molecule_type mRNA
#residues 1-150 #label KAL
#cross-references GB:L03346
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE 1-19
20-150 #domain signal sequence #status predicted #label SIG\
#product Ig heavy chain V region #status predicted

```

20-117      #label MAT\
SUMMARY      #domain variable region #label VRG
              #length 150 #checksum 9720

Query Match      68.8% Score 763; DB 2; Length 150;
Best Local Similarity 69.3% Pred. No. 9,21e-103;
Matches 104; Conservative 21; Mismatches 25; Indels 0; Gaps 0;

Db 1 MEMSWIFLLSLGAGVSEVLOQFGAEVLPKGTSVYISKASGYITTDYNDMVKOSH 60
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 MECSWVFLFLSLITGVHSAVLOQSGAEVLRSGASVYKSCASGYTLTSYMHVVKQTP 60
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 61 GKSLEWIDIDPNFDSSTYKQFKGATLVYDKSSNTAYMELRSTSDTAIVYCARGCF 120
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 GOGLEWMINIRPGNDITYNOKFKKASLTADTSSSTAYMOISLTSDSAVYFCARGNW 120
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 121 PYGMDYWGQGTSVYSSAKTTPPYPLAP 150
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 EGALDYWGQGTSVYSSAKTTPPYPLVP 150
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

ENTRY 6
TITLE Ig heavy chain precursor V region (6A4) - mouse
ORGANISM Mus musculus
DATE 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 22-Nov-1996

ACCESSIONS
REFERENCE PS0024
#authors Margel, M.; Eckhardt, A.; Ehret, W.; von Specht, B.U.;
#journal Duchene, M.; Dondoy, H.
#title Gene (1988) 74:335-345
#cross-references Cloning and characterization of cDNAs coding for the heavy
#accession Pseudomonas aeruginosa outer membrane protein I.
#molecule_type PS0024
#residues 1-139 #label MAR
#experimental_source This chain is obtained from an IgG2a monoclonal antibody against
COMMENT Pseudomonas aeruginosa lipoprotein 1.
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin; pyroglyutamic acid
FEATURE
1-19 #domain signal sequence #status predicted #label SIG\
20-139 #domain Ig heavy chain V region #status predicted #label IGV\
-117 #domain immunoglobulin homology #label IMN\
#modified_site pyrrolidone carboxylic acid (Gln) (in
#mature form) #status predicted
SUMMARY #length 139 #molecular-weight 15673 #checksum 3803

Query Match      67.3% Score 746; DB 2; Length 139;
Best Local Similarity 76.3% Pred. No. 6,10e-100;
Matches 106; Conservative 15; Mismatches 16; Indels 2; Gaps 1;

Db 1 MERHWIFLFSVTVAGVSHOVLOQSGAEVLRSGASVYKSCASGYTFTAYMMHWKORP 60
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 MECSWVFLFLSLITGVHSAVLOQSGAEVLRSGASVYKSCASGYTLTSYMHVVKQTP 60
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 61 GOGLEWIGTINPNTGYTEYNQNFKAATLADKSSSTAYMOISLTSDSAVYCTRSY 120
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 GOGLEWIGTINPNTGYTEYNQNFKAATLADKSSSTAYMOISLTSDSAVYCTRSY 120
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 121 NYEGAMDYWGQGTSVYSS 139
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 119 NMEGALDYWGQGTSVYSS 137
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
ENTRY PL0012 #type fragment
TITLE Ig heavy chain precursor V region (F6-3) - mouse (fragment)

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ORGANISM      #formal_name Mus musculus #common_name house mouse
DATE          30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 18-Oct-1996

ACCESSIONS
REFERENCE PL0012
#authors Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.;
#journal Kohler, H.
#title Mol. Immunol. (1988) 25:33-40
#cross-references Structural basis of stimulatory anti-idiotypic antibodies.
#accession Pseudomonas aeruginosa outer membrane protein I.
#molecule_type PS0024
#residues 1-166 #label CHE
#experimental_source anti-phosphorylcholine response.
COMMENT This protein is an anti-idiotypic antibody which induces an
anti-phosphorylcholine response.
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
1-32 #domain signal sequence #status predicted #label SIG\
33-151 #product Ig heavy chain V region #status predicted
#label MAT\
63-67 #region complementarity-determining 1\
82-98 #region complementarity-determining 2\
131-140 #region complementarity-determining 3\
152-166 #domain C region (fragment) #status predicted #label COR

SUMMARY #length 166 #checksum 5824

Query Match      66.9% Score 742; DB 2; Length 166;
Best Local Similarity 68.5% Pred. No. 2,81e-99;
Matches 102; Conservative 20; Mismatches 26; Indels 1; Gaps 1;

Db 17 SWIFLFLSLGAGVSEVLOQSGAEVLRSGASVYKSCASGYRFTDYVMHWKOSNGKS 76
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 4 SWVFLFLSLITGVHSAVLOQSGAEVLRSGASVYKSCASGYTLTSYMHVVKQTPGCG 63
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 77 LEWIGSTNPYIDTYNKENFRGATVVDKSSSTVYQMLNSTSEDSAVYICAREGFGN 136
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 64 LEWIGSTNPYIDTYNKENFRGATVVDKSSSTVYQMLNSTSEDSAVYICAREGFGN 136
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 137 SLDYWGQGTSVYSSAKTTPPYPLAPG 165
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 123 ALDYWGQGTSVYSSAKTTPPYPLVP 151
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
ENTRY H32513 #type complete
TITLE Ig heavy chain precursor V region (BXW16) - mouse
ORGANISM Mus musculus
DATE 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 20-Mar-1998

ACCESSIONS
REFERENCE H32513
#authors Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.;
#journal Noonan, D.J.; Duchosal, M.A.; Dixon, F.J.; Theofilopoulos,
#title J. Clin. Invest. (1988) 82:852-860
#cross-references Immunoglobulin kappa light chain variable region gene complex
#accession organization and immunoglobulin genes encoding anti-DNA
#molecule_type H32513
#residues 1-137 #label KOF
#cross-references autoantibodies in lupus mice.
#accession H32513
#residues 1-137 #label KOF
#cross-references autoantibodies in lupus mice.
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
SUMMARY #length 137 #molecular-weight 15108 #checksum 816

Query Match      65.6% Score 727; DB 2; Length 137;
Best Local Similarity 73.1% Pred. No. 8,57e-97;
Matches 98; Conservative 22; Mismatches 14; Indels 0; Gaps 0;

```


Db	120	YMGCGTSTVTSAAKTPPSPYPLAPCS	146
Oy	126	YMGGISTVTSAAKTPPSPYPLVPDS	152
RESULT	12		
ENTRY		HYMSG7	#type complete
TITLE		Ig heavy chain precursor V region (93G7, 36-65) - mouse	
ORGANISM		#formal_name Mus musculus #common_name mouse	
DATE		18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 20-Mar-1998	
ACCESSIONS		A94264: A91261; A02028	
REFERENCE		A94264	
#authors		Sims, J.; Rabbitts, T.H.; Estess, P.; Slaughter, C.; Tucker, P.W.; Capra, J.D.	
#journal		Science (1982) 216:309-311	
#title		Somatic mutation in genes for the variable portion of the immunoglobulin heavy chain.	
#cross-references		MUTID:82152618	
#accession		A94264	
#molecule_type		mRNA	
##residues		1-140 #label SIM	
#cross-references		GB:J00493; NID:g195006; PID:g195007	
#experimental_source		strain A/J, hybridoma 93G7	
REFERENCE		A91261	
#authors		Sleekyetz, M.; Gefer, M.L.; Brodeur, P.; Riblet, R.; Marshak-Rothstein, A.	
#journal		Eur. J. Immunol. (1982) 12:1023-1032	
#title		The genetic basis of antibody production: the dominant anti-arsonate idiotype response of the strain A mouse.	
#cross-references		MUTID:83131846	
#accession		A91261	
#molecule_type		DNA	
##residues		20-76, 'TK', '79-118, 'V', '120-125, 'V', '127-134, 'T', '136-140	
#label		SIE	
##cross-references		GB:M19292; NID:g196201; PID:g196202	
#experimental_source		strain A/J, hybridoma 36-65	
##note		The sequence was determined from the differentiated gene from analysis of the sizes of several other	
##note		differentiated genes that hybridize to this one, the authors conclude that all of these V regions have	
		rearranged to the same J segment, JH2	
GENETICS		16/1	
#introns		#superfamily immunoglobulin V region; immunoglobulin homology heterotetramer; hybridoma; immunoglobulin	
CLASSIFICATION			
KEYWORDS			
FEATURE			
19		#domain signal sequence #status predicted #label SIG\	
-140		#product Ig heavy chain V region (93G7) #status predicted #label MAT\	
34-117		#domain immunoglobulin homology #label IMM\	
41-115		#disulfide bonds #status predicted	
SUMMARY		#length 140 #molecular_weight 15514 #checksum 6215	
Query Match		63.9%: Score 709; DB 1; Length 140;	
Best Local Similarity		73.0%: Pred. No. 8.15e-94;	
Matches	100;	Conservative	19; Mismatches 15; Indels 3; Gaps 2;
Db	4	SPITFLFLSTAGVHSEVLOQSGALVNRAGSSVYKSCASGTYTTSIGIMVYKORPQG	63
Oy	4	SWVELFLSTITGTSOAYLQOQSGALVNRAGSSVYKSCASGTYTTSIMVHWYKOTPPQG	63
Db	64	LEWIGYINPNGYNYVNEKFKGKTTLTVKSSSTAYMOLRSITSDSAVYFCARSHYGG	123
Oy	64	LEWIGNIFPNQNDYNYKQKFKASLTADTSSSTAYMQLSSITSDSAVYFCARSHW-EG	122
Db	124	SYDEYDWGGGTPLTVSS	140
Oy	123	A-LDYWGQGTSTVTVSS	137
RESULT	13		
ENTRY		S21810	#type complete

[illegible]

Qy	4	SWVELFLSLITTTGHSOAUYLDQSGAEIYRSGASVKMSCKASGYTLTSTYNNHMYKQPLTGGG	63
Db	64	LEWIGYINPGGAYKKYNEKFKGRKTLTYVDKSSSTAYUOLKSLTSEDSAYVFCARSYVGG	123
Qy	64	LEWIGNIFPGGDDIYUOKFKGRKSLTADTSSSTAYUOLSLTSEDSAYVFCARG-NMEG	122
Db	124	SYFEDYWGQGFTLTVSS	140
Qy	123	A--LDYMGQGTSTVSS	137

RESULT	ENTRY	TITLE	ORGANISM	DATE
15	PH1489	#type fragment Ig heavy chain V region (clone X41-2) - mouse	#formal_name Mus musculus #common_name mouse	03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 1

ACCESSIONS	
PH1489	
PH1482	
SEQUENCE	
Authors	Giusti, A.M.; Manser, T.
#journal	J. Exp. Med. (1993) 177:797-809
#title	Hypermutation is observed only in antibody H chain V region

```
#accession      PH1489
#status         translation not shown
#molecule_type mRNA
```

```

CLASSIFICATION
KEYWORDS
FEATURE
34-117
SUMMARY
#domain immunoglobulin homology #label IMM
#length 140 #Checksum 5044
heterotetramer; immunoglobulin homology

```

Search completed: Thu Apr 15 18:01:18 1999
Job time : 22 secs.

 MUSE (TM)

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MPearch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Thu Apr 15 17:57:49 1999; Maspar time 8.66 Seconds
 at output not generated. 627.099 Million cell updates/sec

Title: >US-08-836-455-2
 Description: (1-145) from US08836455.pep
 Perfect Score: 1019
 Sequence: 1 MGAPAQILIGFLILFPGTRC.....IKRADAPVTSIFPPSKRG 145

Scoring table: PAM 150
 Gap 11

Searched: 116695 segs, 37453910 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: p1r58
 1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 42.409; Variance 104.536; scale 0.406

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	ID	Description	Pred. No.
1	838	82.2	130	1	KVMSM4	Ig kappa chain precur	7.84e-116
2	690	67.7	106	2	PL0260	Ig kappa chain V regi	4.05e-91
3	688	67.5	106	2	PL0259	Ig kappa chain V regi	8.65e-91
4	686	67.3	234	2	SL4237	Ig kappa chain precur	1.87e-90
5	670	65.8	129	2	D32513	Ig kappa chain precur	8.40e-88
6	647	63.5	106	2	PL0262	Ig kappa chain precur	5.39e-84
7	645	63.3	117	1	KVMSJB	Ig kappa chain V regi	1.15e-83
8	640	62.8	234	2	S01320	Ig kappa chain precur	7.74e-83
9	632	62.0	129	2	S40369	Ig kappa chain - huma	1.62e-81
10	622	61.0	125	2	S40353	Ig kappa chain V-J-C	7.25e-80
11	622	61.0	141	2	A49134	Ig kappa chain V-1 re	7.25e-80
12	619	60.7	230	2	S33161	Ig kappa chain - shee	2.26e-79
13	615	60.4	123	2	S40313	Ig kappa chain V-J re	1.03e-78
14	615	60.4	129	2	B23986	Ig kappa chain precur	2.15e-77
15	614	60.3	98	2	PH1062	Ig light chain V regi	1.51e-78
16	614	60.3	108	4	B47271	nitrophenyl phosphon	1.51e-78
17	612	60.1	128	2	A26406	Ig kappa chain V regi	3.23e-78
18	610	59.9	129	2	S40317	Ig kappa chain - huma	6.89e-78
19	609	59.8	132	2	S40334	Ig kappa chain - huma	1.01e-77
20	607	59.6	127	2	PH1224	Ig kappa chain precur	2.15e-77
21	601	59.0	125	2	S40349	Ig kappa chain V-J re	2.09e-76
22	599	58.8	127	2	S52447	Ig kappa chain V regi	4.45e-76
23	598	58.7	130	2	S40368	Ig kappa chain - huma	6.50e-76

24	596	58.5	126	2	A34904	Ig kappa chain precur	1.39e-75
25	589	57.8	135	2	S24320	Ig kappa chain precur	1.96e-74
26	588	57.7	125	2	S40315	Ig kappa chain - huma	2.86e-74
27	588	57.7	127	2	S40367	Ig kappa chain V-J-C	2.86e-74
28	586	57.5	122	2	A29380	Ig kappa chain precur	6.10e-74
29	585	57.5	125	2	S40333	Ig kappa chain V-J re	6.10e-74
30	584	57.3	131	2	S40352	Ig kappa chain V-J-C	1.30e-73
31	583	57.2	115	2	UL0080	Ig kappa chain precur	1.90e-73
32	583	57.2	129	2	S52793	Ig kappa chain V regi	1.90e-73
33	583	57.2	139	2	S52789	Ig kappa chain V regi	1.90e-73
34	583	57.2	129	2	S40365	Ig kappa chain - huma	1.90e-73
35	582	57.1	126	2	S40335	Ig kappa chain V-J-C	2.77e-73
36	581	57.0	128	1	KVMS11	Ig kappa chain precur	4.04e-73
37	580	56.9	88	2	PL0261	Ig kappa chain V regi	5.89e-73
38	580	56.9	129	2	S40332	Ig kappa chain - huma	5.89e-73
39	579	56.8	128	2	S46372	Ig light chain variab	8.60e-73
40	578	56.7	132	2	PL0101	Ig kappa chain precur	1.25e-72
41	578	56.5	128	2	S38646	Ig kappa chain V regi	2.67e-72
42	576	56.3	101	2	B28840	Ig kappa chain V regi	5.68e-72
43	574	56.3	127	2	S11240	Ig kappa chain V regi	5.68e-72
44	573	56.2	101	2	C28840	Ig kappa chain V regi	8.29e-72
45	571	56.0	123	2	S40331	Ig kappa chain - huma	1.76e-71

ALIGNMENTS

RESULT 1

ENTRY KVMSM4 #type complete
 TITLE Ig kappa chain precursor V region (MOPC 41) - mouse
 CONTAINS Ig kappa chain precursor V region VK41
 ORGANISM #formal_name Mus musculus #common_name house mouse
 DATE 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 16-Aug-1996

ACCESSIONS A93211; A93815; A94239; A01922; A01923
 REFERENCE A93211
 #authors Seidman, J.G.; Max, E.E.; Leder, P.
 #journal Nature (1979) 280:370-375
 #title A kappa-immunoglobulin gene is formed by site-specific recombination without further somatic mutation.
 #cross-references MOPC:79221900
 #accession A93211
 ##molecule-type DNA
 ##residues 1-130 ##label PC41
 #accession B93211
 ##molecule-type DNA
 ##residues 1-117 ##label VK41
 ##note the sequences were determined from the differentiated gene MOPC 41 and the germline gene VK41

REFERENCE A93815
 #authors Burstein, Y.; Schechter, I.
 #journal Proc. Natl. Acad. Sci. U.S.A. (1977) 74:716-720
 #title Amino acid sequence of the NH-2-terminal extra piece segments of the precursors of mouse immunoglobulin lambda-1-type and kappa-type light chains.
 #cross-references MOPC:77148916
 #accession A93815
 ##molecule-type protein
 ##residues 1-33 ##label BUR
 ##note Met-3 is apparently used as an alternative initiator in 25% of the chains

REFERENCE A94239
 #authors Gray, W.R.; Dreyer, W.J.; Hood, L.
 #journal Science (1967) 155:465-467
 #title Mechanism of antibody synthesis: size differences between mouse kappa chains.
 #cross-references MOPC:67056897
 #accession A94239
 ##molecule-type protein
 ##residues 23-49, 'B', '51-53', 'LSB', '57-58', 'zz', '61-62', 'B2', '65-76', 'B', '78-108, 110-130 ##label GRA
 ##note #experimental_source Bence Jones protein MOPC 41

GENETICS
 #introns 19/1

Complex	Accessions	Reference	Journal Title	Accessions	Reference	Journal Title
COMPLEX						
An immunoglobulin heterotetramer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.						
CLASSIFICATION						
KEYWORDS						
FEATURE						
1-22						
3-22						
23-130						
38-112						
45-110						
SUMMARY						
Query Match						
Best Local Similarity 92.2%: Score 838; DB 1; Length 130;						
Matches 118; Conservative 4; Mismatches 6; Indels 0; Gaps 0;						
Db	3	MRADAQIFGELLFPQTRCDIQMTGSPSSLSASLGERVSLTCRASODIGSSIMNIQOEP	62			
QY	1	MGAPAQIIGFLLFPETRCDIQMTGSPSSLSASLGERVSLTCRASODIGIMLHNIQOEP	60			
Db	63	DGTRKRLIVATSSLDGVPKRFSGSSAGSYSLTITSSLEDFVDYICLQYASSPWRTGG	122			
QY	61	DGTRKRLIVATSSLDGVPKRFSGSSAGSYSLTITSSLEDFVAYCLOQYASSPWRTGG	120			
Db	123	GTKLEIKR 130				
QY	121	GTKLEIKR 128				
RESULT	2					
ENTRY						
TITLE						
ORGANISM						
DATE						
ACCESSIONS						
REFERENCE						
authors						
Journal Title						
#cross-references M01D:90111618						
#accession						
KEYWORDS						
FEATURE						
1-23						
24-34						
35-49						
50-56						
57-88						
89-97						
98-106						
SUMMARY						
Query Match						
Best Local Similarity 93.4%: Pred. No. 4; 0.5e-91;						
Matches 99; Conservative 3; Mismatches 4; Indels 0; Gaps 0;						
Db	1	DIQMTGSPSSLSASLGERVSLTCRASODIGSSIMNIQOEPDGTRKRLIVATSSLDGVPK	60			
QY	21	DIQMTGSPSSLSASLGERVSLTCRASODIGIMLHNIQOEPDGTRKRLIVATSSLDGVPK	80			

[illegible]

[illegible]

TITLE Ig kappa chain precursor - mouse
ORGANISM Mus musculus #common_name house mouse
DATE 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change
10-Sep-1997

ACCESSIONS S01320
REFERENCE S01320
#authors de Maessle, P.; Feys, V.; van de Voorde, A.; Molemans, F.;
Fiers, W.

#journal Eur. J. Biochem. (1988) 176:287-295
#title Expression in non-lymphoid cells of mouse recombinant
immunoglobulin directed against the tumour marker human
placental alkaline phosphatase.
#cross-references EMBL:X13187; NID:951784; PID:951785
#accession S01320
#molecule_type mRNA
#residues 1-234 #label DE1
#cross-references EMBL:X13187; NID:951785
#note this sequence was determined from the differentiated
gene

ORDS heterotrimer; immunoglobulin
FEATURE 1-20
21-234 #domain signal sequence #status predicted #label SIG
SUMMARY #product Ig kappa chain #status predicted #label MAT
#length 234 #molecular_weight 25920 #checksum 6431

Query Match 62.8%; Score 640; DB 2; Length 234;
Best Local Similarity 60.6%; Pred. No. 7,74e-83;
Matches 86; Conservative 28; Mismatches 28; Indels 0; Gaps 0;

Db 1 MSVPTQVGLLLMLTPARCDIQMTQSPASISVSGESVITTCRASENYSNLAWYQKQ 60
QY 1 MGAPAQILGFLFLFPGRCDIQMTQSPSSLSASLGQVSLTCRASQDIGINLHMLQGP 60
Db 61 GKSPQLVYATKVDYPSRFSGSGSTQYSLKINSIQSDPFGSYTCQHWDPPTFGS 120
QY 61 DGTIKRLIYATSSLSGSGVPRFSGSGSDYSLTISLSEDFVAYYCLQYASSPYTFGG 120

Db 121 GTKLEMRADAPTVSIFPPSS 142
QY 121 GTKLEIRADAPTVSIFPPSS 142

RESULT 9
ENTRY S40369 #type complete
TITLE Ig kappa chain - human
ORGANISM Mus musculus #formal_name Homo sapiens #common_name man
06-Mar-1994 #sequence_revision 26-May-1995 #text_change
08-Sep-1997
ACCESSIONS S40369
REFERENCE S40312
#authors Klein, R.; Jaenichen, R.; Zachau, H.G.
#journal Eur. J. Immunol. (1993) 23:3248-3271
#title Expressed human immunoglobulin chi genes and their
hypermutation.
#accession S40369
#status preliminary; translation not shown
#molecule_type mRNA
#residues 1-129 #label KIE
#cross-references EMBL:X72479; NID:9441426; PID:9441427
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotrimer; immunoglobulin
SUMMARY #length 129 #molecular_weight 14063 #checksum 6277

Query Match 62.0%; Score 632; DB 2; Length 129;
Best Local Similarity 68.8%; Pred. No. 1.62e-81;
Matches 88; Conservative 20; Mismatches 20; Indels 0; Gaps 0;

Db 2 MRVLAOLGLLCEPARCDIQMTQSPSSLSASVGDRTVITCRASHYISNHLWYFQKP 61
QY 1 MGAPAQILGFLFLFPGRCDIQMTQSPSSLSASLGQVSLTCRASQDIGINLHMLQGP 60
Db 62 GKAPKSLIYATSSLSGSGVPRFSGSGSTQYSLKINSIQSDPFGSYTCQHWDPPTFGS 121
QY 62 GKAPKSLIYATSSLSGSGVPRFSGSGSTQYSLKINSIQSDPFGSYTCQHWDPPTFGS 121

QY 61 DGTIKRLIYATSSLSGSGVPRFSGSGSDYSLTISLSEDFVAYYCLQYASSPYTFGG 120
Db 122 GTKLEIR 129
QY 121 GTKLEIR 128

RESULT 10
ENTRY S40353 #type complete
TITLE Ig kappa chain V-J-C region - human
ORGANISM Mus musculus #formal_name Homo sapiens #common_name man
19-May-1994 #sequence_revision 26-May-1995 #text_change
20-Mar-1998
ACCESSIONS S40353
REFERENCE S40312
#authors Klein, R.; Jaenichen, R.; Zachau, H.G.
#journal Eur. J. Immunol. (1993) 23:3248-3271
#title Expressed human immunoglobulin chi genes and their
hypermutation.
#accession S40353
#status preliminary; translation not shown
#molecule_type mRNA
#residues 1-125 #label KIE
#cross-references EMBL:X72463
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotrimer; immunoglobulin
SUMMARY #length 125 #molecular_weight 13441 #checksum 9514

Query Match 61.0%; Score 622; DB 2; Length 125;
Best Local Similarity 68.3%; Pred. No. 7.25e-80;
Matches 84; Conservative 22; Mismatches 17; Indels 0; Gaps 0;

Db 1 LUGLLIMFPGARCDIQMTQSPSSLSASVGDRTVITCRASQIGNDLGWYQKPKAPKR 60
QY 7 ILGFLFLFPGRCDIQMTQSPSSLSASLGQVSLTCRASQDIGINLHMLQGPDPGTR 66
Db 61 LIYATSSLSGSGVPRFSGSGSTQYSLKINSIQSDPFGSYTCQHWDPPTFGS 120
QY 67 LIYATSSLSGSGVPRFSGSGSDYSLTISLSEDFVAYYCLQYASSPYTFGGTKLEI 126

Db 121 KRT 123
QY 127 KRA 129

RESULT 11
ENTRY A49134 #type fragment
TITLE Ig kappa chain V-I region (ISE) - human (fragment)
ORGANISM Mus musculus #formal_name Homo sapiens #common_name man
19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change
08-Sep-1997
ACCESSIONS A49134; S25115
REFERENCE A49134
#authors Rocca, A.; Khamilchi, A.A.; Aucoeur, P.; Noel, L.H.;
Denoroy, L.; Preud'homme, J.L.; Cogné, M.
#journal Clin. Exp. Immunol. (1993) 91:506-509
#title Primary structure of a variable region of the V kappa I
subgroup (ISE) in light chain deposition disease.
#cross-references EMBL:93185310
#accession A49134
#status preliminary
#molecule_type mRNA; protein
#residues 1-141 #label ROC
#cross-references EMBL:X67322; NID:933268; PID:933269
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotrimer; immunoglobulin
SUMMARY #length 141 #checksum 3566

Query Match 61.0%; Score 622; DB 2; Length 141;
Best Local Similarity 61.2%; Pred. No. 7.25e-80;
Matches 85; Conservative 28; Mismatches 26; Indels 0; Gaps 0;

[illegible]

SUMMARY #length 98 #checksum 6933

Query Match 60.38; Score 614; DB 2; Length 98;
 Best Local Similarity 87.88; Pred. No. 1.5le-78;
 Matches 86; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Db 1 DIQMTQSPSSLSASLGKRVSLTCRASQEIISGYLWLGQKPDGTIKRLIYSTSTLNSGVPR 60
 |||||1|||||:|||||:| ||| |||||:|:| |||||
 QY 21 DIQMTQSPSSLSASLGKRVSLTCRASQDIGINLHWLQGEEDGTIKRLIYATSSLSGSGVPR 80
 |||||1|||||:|||||:| ||| |||||:|:| |||||
 Db 61 RPSGSRSGSDYSLTISLSEDFADYCYCLOYASSPYTF 98
 |||||1|||||:|||||:| ||| |||||:|:| |||||
 QY 81 RPSGSRSGSDYSLTISLSEDFVAYCYCLOYASSPYTF 118

Search completed: Thu Apr 15 17:58:14 1999
 Job time : 25 secs.

Query Match	67.4%;	Score 293;	DB 8;	Length 1605;
Best Local Similarity	93.7%;	Pred. No. 3.73e-189;		
Matches 314;	Conservative 0;	Mismatches 21;	Indels 0;	Gaps

CC R78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45
CC and in the claims are different from the descriptions in the
CC sequence listings. The descriptions in the sequence listings are

CC and in the claims are different from the descriptions in the CC sequence listings. The descriptions in the sequence listings are used here.

CC variable region of a particular antibody polypeptide was also used
 CC for PCR amplification of that variable region, in conjunction with
 CC an appropriate V-region primer. In addition, the VH primer Q97518
 CC was used to amplify the mab 2D5 and 5B6 heavy chains. The sequences
 CC of the PCR amplified nucleotides were determined. These are given
 CC in Q97498-097510 and the deduced AA sequences in R79241-R79250 &
 CC R78970-R78971. The descriptions of the SEQ ID nos given on pp 44-45
 CC and in the claims are different from the descriptions in the
 CC sequence listings. The descriptions in the sequence listings are
 CC used here.

CC Sequence 321 BP; 82 A; 80 C; 72 G; 87 T;

Query Match 65.3%; Score 284; DB 15; Length 321;

Best Local Similarity 94.4%; Pred. No. 1.40e-182;

Matches 302; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Db 1 gacatccagatgacccagctccatccctctatctgctctctggaagaagatcact 60
 |||||||
 61 GACATCCAGATGACCCAGCTCCATCCTCTTCTGCGCTCTGGACAAAGTCACT 120
 |||||||
 Db 61 ctcaactgtcggcgcaagtcagacattgtagttaaactgctcaagtcgaacca 120
 |||||||
 121 CTCACCTTGCGGGCAAGTCAAGACATGTGATTAATTAATTAATTAATTAATTA 180
 |||||||
 Db 121 gatggaactataaagcctgactcagccatcgatcggttttagattctggtcccaaa 180
 |||||||
 181 GATGGAACATTAATTAAGCCTGATTAAGCCACATCAAGTTAAGTTGCTGCTCCCAA 240
 |||||||
 Db 181 aggttcagtgagcagtagtctggtcagattatctctccacacaaagcctgagct 240
 |||||||
 241 AGGTTCAGTGAGCAGTAGCTGCTGGTCAGATTAATTAATTAATTAATTAATTA 300
 |||||||
 Db 241 gaagatttgtagactactactgctcacaatgtcttaattctcgtacacgttcgaagg 300
 |||||||
 301 GAAGATTGTGTACCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 360
 |||||||
 Db 301 gggaccaagctggaataaa 320
 |||||||
 QY 361 GGGACCAAGCTGGAATTA 380

RESULT 10

ID 015114 standard; DNA: 432 BP.

AC 015113:

DT 16-MAR-1992 (first entry)

DE IL-2 chimeric antibody light chain clone 447.

OS Interleukin-2; immunosuppressant.

OS Chimeric Homo sapiens.

OS Chimeric Mus musculus.

OS Key cds location/Qualifiers

FT signal_peptide 1..60 /tag= a

FT mat_peptide 61..432 /tag= b

FT mat_peptide 61..432 /tag= c

PN EP-460674-A.

PD 11-DEC-1991.

PF 06-JUN-1991; 109303.

PR 08-JUN-1990; DE-018442.

PA (BOE) BOEHRINGER MANNHEIM GMBH.

PI Weidle U, Kaluza B, Knapp W;

DR WPT: 91-363168/50.

P-PSDB: R15321.

PT New recombinant DNA encoding chimeric antibody - with human

PT constant and non-human variable regions, esp. directed against

PT interleukin 2 receptor

PS Disclosure: Page 11; 24pp; German.

CC The sequence encodes the interleukin-2 (IL-2) chimeric antibody light

CC chain clone 447. Antibodies against IL-2 receptors are useful as

CC immunosuppressants, and are much less immunogenic than mouse or

CC rat antibodies. The DNA sequence provides much higher yields of

CC chimeric antibodies than known methods. See also Q15114-Q15118.

SEQ Sequence 432 BP; 106 A; 102 C; 104 G; 120 T;

Query Match 57.0%; Score 248; DB 3; Length 432;

Best Local Similarity 78.8%; Pred. No. 2.36e-156;

Matches 339; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

Db 1 atgagtgctctgctcagctcttctgcatctctgtgtgcttggttcccaagatgt 60
 |||||||
 1 ATGGAGGCTCTGCTCAGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
 |||||||
 Db 61 gacatccatgacccatccatccatccatccatccatccatccatccatccatccatcc 120
 |||||||
 61 GACATCCATGACCCAGCTCCATCCTCTTATCTGCTCTCTGGACAAAGTCACT 120
 |||||||
 Db 121 atcaacttgccatgcaagtcagggcattagaagtaatatagtggttggaagagaacca 180
 |||||||
 121 CTCACCTTGCGGGCAAGTCAAGACATGTGATTAATTAATTAATTAATTAATTA 180
 |||||||
 Db 181 gggaaatcattaaagggcctgactatcatcagaaaccaacttggaagaggtccatca 240
 |||||||
 181 GATGGAACATTAATTAAGCCTGATTAAGCCACATCAAGTTAAGTTGCTGCTCCCAA 240
 |||||||
 Db 241 cgttcagtgagcagtaggactcaggaagaattatctctcagacatcagcagcctggaatc 300
 |||||||
 241 AGGTTCAGTGAGCAGTAGCTGCTGGTCAGATTAATTAATTAATTAATTAATTA 300
 |||||||
 Db 301 gaagatttgacagactactactgctgacagtagtctcagttctcctcagacgttcgtag 360
 |||||||
 301 GAAGATTGTGTACCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 360
 |||||||
 Db 361 ggcaccaagctggaatacaagggctgctgctgacacacacgtatccatctccacca 420
 |||||||
 361 GGCACCAAGCTGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 420
 |||||||
 Db 421 tccagtgagc 430
 |||||||
 QY 421 TCCAGTAGC 430

RESULT 11

ID 015113 standard; DNA: 432 BP.

AC 015113:

DT 16-MAR-1992 (first entry)

DE IL-2 chimeric antibody light chain 179.

KW Interleukin-2; immunosuppressant.

OS Chimeric Homo sapiens.

OS Chimeric Mus musculus.

OS Key cds location/Qualifiers

FT signal_peptide 1..60 /tag= a

FT mat_peptide 61..432 /tag= b

FT mat_peptide 61..432 /tag= c

PN EP-460674-A.

PD 11-DEC-1991.

PF 06-JUN-1991; 109303.

PR 08-JUN-1990; DE-018442.

PA (BOE) BOEHRINGER MANNHEIM GMBH.

PI Weidle U, Kaluza B, Knapp W;

DR WPT: 91-363168/50.

P-PSDB: R15321.

PT New recombinant DNA encoding chimeric antibody - with human

PT constant and non-human variable regions, esp. directed against

PT interleukin 2 receptor

PS Disclosure: Page 10; 24pp; German.

CC The sequence encodes the interleukin-2 (IL-2) chimeric antibody light

CC chain clone 179. Antibodies against IL-2 receptors are useful as

CC immunosuppressants, and are much less immunogenic than mouse or

CC rat antibodies. The DNA sequence provides much higher yields of

CC chimeric antibodies than known methods. See also Q15114-Q15118.

Sequence 432 BP; 107 A; 101 C; 105 G; 119 T;


```
Db 82 gacatcaagatgacccagctccatctccatctgatatgatacctcagaagagaagtcacg 141
|||||
QY 61 GACATCCAGATGACCCAGCTCCATCCCTTATCTGCTGCTGGGCAAGAGTCAGT 120
142 atcaatcgaagcgagtcagacatgaatgattatgaattgattcccaagaagaca 201
|||||
QY 121 CTCACCTTGCGGCAAGTACGACATTTGTTATTACTTACCTTGGCTTCACAGAGAACCA 180
202 gggaatctcctaagaccctgatactatcgtgcaaatagatgatagatgagggctccatca 261
QY 181 GATGGAACATTTAAACGCTGATCTGATCCACATCCAGTTTAGTTGATGTCGCCAAA 240
Db 262 aggttcagtcgacgttgatctggcgcaagttactctcaccatcagaagccctggataat 321
QY 241 AGGTTCACTGCGCAGTAGGCTGCGGTCACATATTCTCTCACATCAGCAGCTTGAGTCT 300
Db 322 gaagataagggaactatattgtctacagttgatagttcctggatctgctgagtg 381
301 GAAGATTTTGTAGCCTATTACTGTCTACAAATATGCTAGTTCTCCCTACACGTTCCGAGGG 360
Db 382 ggcacaaagctggaatacaacaggcgctgctgacccaactgctccatctccacaca 441
QY 361 GGACACCAAGCTGGAATATAAACGGGCTGATGCTGCACCACTGTATCATCTCCACACA 420
Db 442 tccagat 447
QY 421 TCCAGT 426

RESULT 14
ID T99434 standard; cDNA; 447 BP.
AC T99434;
DT 27-APR-1998 (first entry)
DE Anti-idiotype antibody 3H1 light chain variable region cDNA.
KW Anti-idiotype antibody 3H1; carcinoembryonic antigen; CEA;
KM tumour-specific antigen; tumour; colorectal cancer; lung cancer;
OS Mus musculus.
FH Key Location/Qualifiers
FT CDS 22..447
FT CD5 /*tag= a
PN WO9738725-A1.
PD 23-OCT-1997.
PE 11-APR-1997; U05953.
PR 09-APR-1997; US-631085.
PR 12-APR-1996; US-631085.
PR (KENT ) UNIV KENTUCKY.
PI Chatterjee M, Chatterjee SK, Foon KA;
WP1: 97-526218/48.
DR P-PSDB; W26727.
PT Use of anti-idiotype antibody 3H1 - for delaying development of
PT carcinoembryonic antigen associated tumours
PS Disclosure: Page 38; 66pp; English.
CC This cDNA sequence includes a coding region for the VH region (see
CC variable region (VL) (see W26728) of murine monoclonal anti-idiotype
CC antibody 3H1. A cDNA sequence (see T99435) for the VH region (see
CC W26729) is also provided. These clones can be utilised in the
CC recombinant production of 3H1 polypeptides. 3H1 induces a specific
CC immune response against a distinct and specific epitope of
CC carcinoembryonic antigen (CEA), a tumour-associated antigen. The
CC invention provides methods of delaying development of CEA-associated
CC tumours using 3H1, particularly in high-risk individuals. The
CC method can be used to delay the development of a variety of tumours,
CC including colorectal, gastric and pancreatic tumours, as well as
CC other adenocarcinomas such as those of the breast and lung, and
CC biliary cancer, and gynaecological cancers.
SQ Sequence 447 BP; 118 A; 101 C; 102 G; 126 T;

Query Match 52.4%; Score 228; DB 38; Length 447;
Best Local Similarity 76.8%; Pred. No. 7.81e-142;
Matches 327; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

Db 22 atggtatccacagcctcactctctgtatctgtgctgtgtccaggtatacaatct 81
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QY 1 ATGGGGGCCCCCTCGATCTTGAGTTCTGTGCTGTGTTCCAGGTACCATGATGT 60
Db 82 gacatcaagatgacccagctccatctccatctgatatgatacctcagaagagaagtcacg 141
|||||
QY 61 GACATCCAGATGACCCAGCTCCATCCCTTATCTGCTGCTGGGCAAGAGTCAGT 120
142 atcaatcgaagcgagtcagacatgaatgattatgaattgattcccaagaagaca 201
|||||
QY 121 CTCACCTTGCGGCAAGTACGACATTTGTTATTACTTACCTTGGCTTCACAGAGAACCA 180
202 gggaatctcctaagaccctgatactatcgtgcaaatagatgatagatgagggctccatca 261
QY 181 GATGGAACATTTAAACGCTGATCTGATCCACATCCAGTTTAGTTGATGTCGCCAAA 240
Db 262 aggttcagtcgacgttgatctggcgcaagttactctcaccatcagaagccctggataat 321
QY 241 AGGTTCACTGCGCAGTAGGCTGCGGTCACATATTCTCTCACATCAGCAGCTTGAGTCT 300
Db 322 gaagataagggaactatattgtctacagttgatagttcctggatctgctgagtg 381
QY 301 GAAGATTTTGTAGCCTATTACTGTCTACAAATATGCTAGTTCTCCGTCACAGTTCCGAGGG 360
Db 382 ggcacaaagctggaatacaacaggcgctgctgacccaactgctccatctccacaca 441
QY 361 GGACACCAAGCTGGAATATAAACGGGCTGATGCTGCACCACTGTATCATCTCCACACA 420
Db 442 tccagat 447
QY 421 TCCAGT 426

RESULT 15
ID T34541 standard; cDNA; 447 BP.
AC T34541;
DT 11-OCT-1996 (first entry)
DE Monoclonal anti-idiotype antibody 3H1 VL cDNA.
KW Anti-idiotype antibody; monoclonal antibody; CEA;
KM carcinoembryonic antigen; tumour-associated antigen; cancer;
OS Mus sp.
FH Key Location/Qualifiers
FT CDS 22..447
FT CD5 /*tag= a
PN WO9620219-A2.
PD 04-JUL-1996.
PE 28-DEC-1995; U17105.
PE 28-DEC-1994; US-365484.
PE (KENT ) UNIV KENTUCKY.
PI Chatterjee M, Chatterjee SK, Foon KA, Kohler H;
WP1: 96-321809/32.
DR P-PSDB; R93666.
PT Monoclonal anti-idiotype antibody 3H1 - elicits an immune response
PT to carcinoembryonic antigen
PS Example 2; Fig 1A; 102pp; English.
CC A cDNA clone (T34541) codes for the light chain variable region
CC (R93666) of monoclonal anti-idiotype antibody 3H1 (ATCC HB 12003).
CC It was obt'd. by PCR amplification (see also T34545-46) of cDNA
CC derived from 3H1 hybridoma cells. Anti-idiotype antibody 3H1
CC elicits a specific immune response to a unique epitope of
CC carcinoembryonic antigen (CEA) that is not present on other
CC members of the CEA family or on normal adult tissues. 3H1
CC can be used as a vaccine to elicit immune responses in patients
CC with advanced CEA-associated disease or, when labeled, to enhance
CC tumour detection in imaging.
SQ Sequence 447 BP; 118 A; 101 C; 102 G; 126 T;

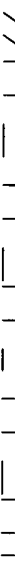
Query Match 52.4%; Score 228; DB 22; Length 447;
Best Local Similarity 76.8%; Pred. No. 7.81e-142;
Matches 327; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

Db 22 atggtatccacagcctcactctctgtatctgtgctgtgtccaggtatacaatct 81
|||||
```

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QY      1 ATGGGGGCCCTGCTCAGATTCTTGGGTTCTTGTGCTCTTGTTCAGGTACAGATGT 60
Db      82 gacatcaagatgaccaggtctccatcttccatglatgcatctctagagagagatcaag 141
QY      61 GACATCCAGATGACCAAGTCACATCCCTTATCTGCTCTCTGGGACAAAGAGTCAGT 120
Db     142 atcacttgcgaagcgagtcagacattaatgttaattggttccacaagaaccca 201
QY     121 CTCACTTGTGCGGCAAGTCAGACATTGGTATTAATTACATTGGCTTCAGCAGGAACCA 180
Db     202 gggaaatctccctaaagacctatctatcgtgcgaatagattgatatagatgggtcccatca 261
QY     181 GATGGAACCTATTAAACGGCTGATCTACGCCACATCCAGTTAGGTTCTGTGTCGCCCAA 240
Db     262 aggttcagtgagcagtgatctgggcaagtttactctccaccatcagcagcctggaatat 321
QY     241 AGGTTCAAGTGGCAGTAGGCTGGGTCAAGATTATCTTCACCATCAGCAGCCTTGAGTCT 300
Db     322 gaagatatgggaacttattatgtctacagtttgatgagttccgltggatgttcggtgga 381
QY     301 GAAGATTTTGTAGCTTATTACTGTCTACAATATGCTAGTCTCCGTACACGTTCCGAGGG 360
Db     382 ggcacccaagctggaatcaaacgggctgagtgcgcaccaactgctcccatctccacca 441
QY     361 GGGACCAAGCTGGAATTAATAACGGGCTGATGCTGCACCAACTGTATCCATCTCCACCA 420
Db     442 tccagct 447
QY     421 TCCAGT 426
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Search completed: Sat Apr 17 14:55:13 1999
Job time : 222 secs.

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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Sat Apr 17 14:28:17 1999; MasPar time 607.76 Seconds
1281.743 Million cell updates/second
lar output not generated.

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Title: >US-08-836-455-1
Description: (1-435) from US08836455.seq
Perfect Score: 435
N.A. Sequence:
Comp: 1 ATGGGAGCCCTTGCTCAGAT.....CACCATCCAGTAACCTTGGG 435
TACCCCTGGGGAGCGAGGTCTA.....GTGGTAGGTCTATCGAACCC

```

Scoring table: TABLE default

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Nmatch  STD :  Dbase 0;  Query 0
```

Searched: 2275026 seqs, 895388244 bases x 2

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Post-processing: Minimum Match 0%
Listing first 45 summaries
```

```
Database:      emb1-est56
               1:em_est1 2:em_gss1 3:em_gss2 4:em_gss3
Database:      genbank-est109
```

5:9**pb** **est1** 6:9**pb** **est10** 7:9**pb** **est11** 8:9**pb** **est12** 9:9**pb** **est13**
10:9**pb** **est14** 11:9**pb** **est15** 12:9**pb** **est16** 13:9**pb** **est17**
14:9**pb** **est18** 15:9**pb** **est19** 16:9**pb** **est2** 17:9**pb** **est10**
18:9**pb** **est21** 19:9**pb** **est3** 20:9**pb** **est4** 21:9**pb** **est5** 22:9**pb** **est6**
23:9**pb** **est7** 24:9**pb** **est8** 25:9**pb** **est9** 26:9**pb** **gsst1** 27:9**pb** **gsst2**
28:9**pb** **gsst3** 29:9**pb** **gsst4**

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list1cs:  Mean 10.183;  Variance 1.785;  scale 5.704
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	175	40.2	393	16	T27593	EST100653 Homo sapiens	0.00e+00
2	167	38.4	413	24	AA330347	EST14279 Testis tumor	0.00e+00
3	164	37.7	382	24	AA295786	EST100987 Pancreas tum	0.00e+00
4	163	37.5	345	25	AA335086	EST39457 Esophagus tum	0.00e+00
5	163	37.5	352	24	AA301261	EST14181 Testis tumor	0.00e+00
6	156	35.9	516	16	R67559	Y142h11.r1 Homo sapien	6.76e-28
7	155	35.6	395	16	T29112	EST69384 Homo sapiens	1.41e-28
8	154	35.4	303	24	AA300891	EST14031 Testis tumor	2.92e-28
9	153	35.2	357	25	AA361497	EST1040 T-cell lympho	6.04e-28
10	151	34.7	303	24	AA300788	EST13648 Testis tumor	2.57e-27
11	143	32.9	282	24	AA300491	EST13404 Testis tumor	7.59e-25
12	141	32.4	301	25	AA377295	EST89887 Small Intesti	3.06e-25
13	140	32.2	334	24	AA327254	EST30547 Colon I Homo	6.13e-25

15	139	32.0	297	24	AA3013343	EST14275	Testis tumor	1.22e-249
14	138	31.7	335	24	AA3183737	EST20620	Spleen i Homo	2.43e-247
16	135	31.0	289	24	AA295508	EST100751	Pancreas tum	1.88e-240
17	132	30.3	286	16	T27581	EST100107	Homo sapiens	1.41e-233
18	126	29.0	286	24	AA3373342	EST30974	Colon i Homo	7.27e-220
19	126	29.0	333	24	AA3007732	EST13847	Testis tumor	7.27e-220
20	125	28.7	281	25	AA366485	EST17625	Pancreas tumor	1.39e-217
21	123	28.3	288	25	AA366847	EST17860	Pancreas tumor	4.98e-213
22	118	27.1	289	24	AA295881	EST101050	Pancreas tum	1.14e-201
23	117	26.9	288	16	T27721	EST33641	Homo sapiens	2.10e-199
24	117	26.9	345	11	AA710291	vt35a04.r1	Barstead mo	1.09e-199
25	116	26.7	405	25	AA345486	EST1505	Gall bladder	3.87e-197
26	114	26.2	438	15	R64893	Y12F09.r1	Homo sapien	1.29e-192
27	109	25.1	400	7	AA456778	zw2F11.r1	Scaris ovar	2.45e-181
28	108	24.8	233	24	AA3374457	EST30844	Colon i Homo	4.34e-177
29	107	24.6	328	24	AA318638	EST20808	Spleen i Homo	7.67e-177
30	107	24.6	370	24	AA295093	EST100400	Pancreas tum	1.67e-177
31	106	24.4	328	24	AA295311	EST100471	Pancreas tum	1.35e-174
32	106	24.4	451	5	R31304	Yb6a07.r1	Homo sapien	1.35e-174
33	105	24.1	465	16	R69532	Y78b09.r1	Homo sapien	2.36e-172
34	104	23.9	255	24	AA295941	EST101165	Thymus T11 H	4.10e-170
35	104	23.9	323	24	AA3373357	EST30702	Colon i Homo	4.10e-170
36	103	23.7	205	25	AA360654	EST59843	T-cell Lympho	7.10e-168
37	103	23.7	261	5	R46878	Y5j4h03.r1	Homo sapien	7.10e-168
38	103	23.7	261	24	AA294819	EST100059	Pancreas tum	7.10e-168
39	103	23.7	279	24	AA294843	EST100058	Pancreas tum	7.10e-168
40	103	23.7	335	5	R49681	Y55f09.r1	Homo sapien	7.10e-168
41	102	23.4	397	5	R49771	Y55c03.r1	Homo sapien	1.12e-165
42	101	23.2	195	24	AA295956	EST12160	Oterus tumor	2.09e-163
43	101	23.2	196	24	AA301279	EST14202	Testis tumor	2.09e-163
44	101	23.2	241	16	H25952	Y15a07.r1	Homo sapien	2.09e-163
45	99	22.8	125	11	AA717201	vp4a07.r1	Barstead mo	6.03e-153

ALIGNMENTS

RESULT	1	27593	393 bp	mRNA	EST	06-SEP-1995
LOCUS		EST100653	Homo sapiens	CDNA 5', end similar to immunoglobulin kappa light chain, V region (GB:I01279) (HT:3043).		
DEFINITION		27593				
ACCESSION		9609691				
MID		EST.				
KEYWORDS		human primer-M13 Reverse library-Human Pancreas.				
SOURCE		Homo sapiens				
ORGANISM		Eukaryotes; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygia; Channata; Terrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominoidea; Homo.				
REFERENCE		1 (bases 1 to 393)				
AUTHORS		Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fullmer,R.A., Bult,C.J., Lee,N., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Chu,M.-W., Claydon,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fierziger,L.M., Fitzhugh,W.M., Fitchman,J., Geoghegan,N.S.M., Glöckner,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkley Jr.,P.S., Kellay,J.M., Klineck,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palancues,R.F., McDonald,L.A., Nguyen,D.T., Pellegrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Sander,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.-J., Dimke,D., Feng,P., Ferrie,A., Fischer,C., Hastings,G.A., He,W.-W., Hu,Y.-S., Greene,J.M., Guuber,J., Hudson,P., Kim,A., Kozak,D.L., Kunsch,C., Ji,H., Matisner,P.S., Olsen,H., Raymond,L., Wei,Y.-F., Wing,J., Xu,C., Yu,G.-L., Ruben,S.M., Dillon,P.J., Fannon,M.R., Rosen,C.A., Hasseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.				
JOURNAL		Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of cDNA Sequence				
COMMENT		Unpublished (1995)				
		Other_ESTs: THC24356				
		Contact: Venter, JC				
		The Institute for Genomic Research				

Accession	AA295786
MD	g1948121
Keywords	EST.
Source	human.
Organism	homo sapiens
Reference	Eukaryote: mitochondrial eukaryotes; Metazoa: Chordata: Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
Authors	1 (bases 1 to 382)
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Feldner,R.A., Bult,C.J., Lee,N.G., Kirness,E.F., Weinstein,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man'wal,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hynes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodde,A., Gnehm,C.L., Hanna,M.C., Heblom,E., Hinkle,P.S., Jr., Kelley,J.M., Kelley,J.C., Li,H., Li,I., Marmaros,S.M., Merrick,J.M., Moreno-Palmer,R.F., McDonald,L.A., Nguyen,D.T., Peligro,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Uterback,T.R., Weidman,J.F., Li,Y., Bebnarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.F., Ferrie,A.C., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Weissner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,D., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M., and Venter,J.C.	Initial assessment of human gene diversity and expression pattern based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl.), 3-174 (1995)	96026280
Journal	Comment
Medline	
Comment	
Contact: Kerlavage, AR Bioinformatics The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA Tel: 3018699056 Fax: 3018699423 Email: akkerlav@tigr.org For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/cdb/ngi/ngi.html) Seq primer: M13 Reverse.	
Features	
Source	Location/Qualifiers
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Best Local Similarity	73.3%; Pred. No. 0.00e+00;
Matches 261; Conservative	0; Mismatches 94; Indels 1; Gaps 1;
Db	28 ATGAGGTCGCCGCTCAGCTCTTGCGGCTCCTGCTACTGTGCGTCGAGTGCCAGATGT 87
Y	1 ATGGGGGCCCTGCTCAGATCTTGGGTTCTTGTGCTCTGTGTTCCAGGTACAGATGT 60
Db	88 GACATCCGATGACCCAGTCATCTCCCTCCCTGCTCAGCTCTGGGNGACAGATCACC 147
Y	61 GACATCCGATGACCCAGTCATCTCCCTCTTATCTGCTCCTCTCGGGACAAAGATAGT 120
Db	148 ATCACTTCCGCGGAGGTCAAGGCGATTAGCACTTTTAAATTGGTATTCACAGAGACCA 207
Y	121 CTCATCTGTGGGCAAGTCAGACATGTGTTTAAGTTAATTCATTGCGTTCACAGAAACCA 180
Db	208 GGTAAAGCCCTAAAGCTCTGATCTATGACCTCCACAGTTTGCAAGAGTGGGTCCTCATCA 267

Oy	181	GATGACACTTTAAAGCCCTGATCTACGCCACATCCAGTTTAGTTGTGGTGTCCCAAA	240
Db	268	AGGTTTCAGTGGCAGTGGATCTGGGACGAGATTCAGTCTCANCATCAGCAGTCTGCANCAT	327
Oy	241	AGGTTTCAGTGGCAGTGGATCTGGGACGAGATTCAGTCTCANCATCAGCAGTCTGCANCAT	300
Db	328	GAGGTTTTCGCACTACTACTGCTGTACGACGAGTTTACAGTT-TCGTCACAATTTGG	382
Oy	301	GAGATTTTTCGCACTACTACTGCTGTACGACGAGTTTACAGTTTTCGTCACAATTTGG	356
RESULT	4	AA335086	345 bp
LOCUS			EST
DEFINITION		EST339457 Esophagus tumor Homo sapiens cDNA 5' end similar to	21-APR-1997
ACCESSION		AA335086	
KEYWORDS		g1987349	
SOURCE		EST.	
ORGANISM		human.	
		Homo sapiens	
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REFERENCE		Homo.	
AUTHORS		1 (bases 1 to 345)	
		Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Feldner,R.A.,	
		Balt,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,	
		White,O., Sutton,G., Blake,J.A., Brando,R.C., Man-Well,C.,	
		Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,	
		Fitzgerald,L.M., Fitzhugh,W.M., Fitchman,J.L., Georgiades,N.S.,	
		Glocke,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,	
		Kelley,D.M., Kelley,J.C., Liu,L.-T., Marmaros,S.M., Merrick,J.M.,	
		Moreno-Palancques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,	
		Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R.,	
		Small,K.V., Spiggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,	
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		He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K.,	
		Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Melsner,P.S., Olsen,H.,	
		Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,	
		Dillon,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,	
		Fraser,C.M., and Venter,J.C.	
TITLE		Initial assessment of human gene diversity and expression patterns	
JOURNAL		based upon 83 million nucleotides of cDNA sequence	
MEDLINE		Nature 377 (6547 Suppl), 3-174 (1995)	
COMMENT		96026280	
		Other_ESTS: EST39456 TH0167177	
		Contact: Kerlavage, AR	
		Bioinformatics	
		The Institute for Genomic Research	
		9712 Medical Center Drive, Rockville, MD 20850 USA	
		Tel: 3018699056	
		Fax: 3018699422	
		Email: arkerlavage@tigr.org	
		For clone availability, additional sequence and expression	
		information related to this EST, please check the TIGR Human Gene	
		Index (http://www.tigr.org/tdb/hgi.html)	
		Seq primer: M3 Reverse.	
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Matches		246; Conservative 0; Mismatches 83; Indels 0; Gaps 0;	

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 Qy 1 ATGGGGGCCCCCTGCTCAGATTCCTGGGCTTGTGGCTTGTTCAGGATCCAGATGT 60
 Db 66 GACATCCAGATGACCCAGTCTCCATCCCTGCTGTCATGTAGAGAGAGATGACC 125
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 Db 126 ATCACTGCGCGGAGTCAAGCATTAGACCCATTAAATGGTATCAACAAAACCT 185
 121 CTCACCTGTCGGGAGACGACGATTTGTAATTAACCTTACATTAATGCTTACAGAGAACCA 180
 Qy 121 CTCACCTGTCGGGAGACGACGATTTGTAATTAACCTTACATTAATGCTTACAGAGAACCA 180
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 Qy 181 GAGGAGACTATTAACCGCTGATCTACGCCACATCCAGATTGGTTCGTTGCCCAAA 240
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RESULT 5
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 DEFINITION EST14181 Testis tumor Homo sapiens cDNA 5' end similar to
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 AA301261
 ACCESSION g1953592
 NID
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 SOURCE human.
 ORGANISM Homo sapiens
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 Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homnidae;
 Homo.
 1 (bases 1 to 352)
 Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
 Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
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 Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D.,
 Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghegan,N.S.,
 Glodde,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr.,
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 Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Peligrino,S.M.,
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 Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
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 Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M.,
 Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C.,
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 Initial assessment of human gene diversity and expression patterns
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 96026280
 JOURNAL MEDLINE
 COMMENT Other-ESTs: TH167177
 Contact: Kerlavage, AR
 Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Tel: 3018699056
 Fax: 3018699423
 Email: atkerlav@tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please check the TIGR Human Gene
 Index (<http://www.tigr.org/tdb/hgi.html>)
 Seq primer: M3 Reverse.
 Location/Qualifiers

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 /note="Organ: testis; Vector: pBluescript SK-; site_1:
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 /clone_lib="Testis tumor"
 /sex="male"
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BASE COUNT 84 a 94 c 83 g 88 t 3 others
 ORIGIN

Query Match 37.5%; Score 163; DB 24; Length 352;
 Best Local Similarity 75.4%; Pred. No. 0.00e+00;
 Matches 248; Conservative 0; Mismatches 80; Indels 1; Gaps 1;

Db 1 TGAGGGTCCCGGCTCAGCTCCTGGGCTCCTGCTACTCTGCTCCAGTCCAGATGTG 60
 2 TGGGGGCCCCCTGCTCAGATTCCTGGGCTTGTGGCTTGTTCAGGATCCAGATGTG 61
 Qy 2 TGGGGGCCCCCTGCTCAGATTCCTGGGCTTGTGGCTTGTTCAGGATCCAGATGTG 61
 Db 61 ACATCCAGATGACCCAGTCTCCATCCCTGCTGTCATGTAGAGAGATGACC 120
 62 ACATCCAGATGACCCAGTCTCCATCCCTGCTGTCATGTAGAGAGATGACC 121
 Qy 62 ACATCCAGATGACCCAGTCTCCATCCCTGCTGTCATGTAGAGAGATGACC 121
 Db 121 TCACCTGCGGCGGAGTCAAGCATTAGACGATTAAATGGTATCAACAAAACAG 180
 122 TCACCTGCGGCGGAGTCAAGCATTAGATTTAATTAACCTTACATTAATGCTTACAGAGAACCA 181
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 Db 181 GGAAGAGCCCTAAGTCTCCTATCTATGTCATCCAGATTGGCAACAGCGGGTCCCATCA 240
 182 ATGGAAGTATTAACCGCTGATCTACGCCACATCCAGATTGGTTCGTTGCCCAAA 241
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 Db 241 GGTTCAGTGGCAGTGGATCTTGGGACAGATTTCACCTGCTCAGATCAGAGTCCAGACT 300
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 Qy 242 GGTTCAGTGGCAGTGGATCTTGGGACAGATTTCACCTGCTCAGATCAGAGTCCAGACT 300
 Db 301 GAGGCTTTGCAATTAATTAATCTGTCACCA 329
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RESULT 6
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 DEFINITION y142h11.r1 Homo sapiens cDNA clone 141957 5' similar to
 gb:X00965_cds1 IG KAPPA CHAIN PRECURSOR V-I REGION (HUMAN);.
 R67559
 ACCESSION g840197
 NID
 KEYWORDS EST.
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 (Pharmacia) with a modified polylinker host=DHI0B (ampicillin
 resistant) primer=M3RPI Rsitel=Not I Rsitel2=Eco RI Female placenta
 obtained at birth (full term). 1st strand cDNA was primed with a
 Not I - oligo(dT) primer [5'
 AACTGGAAGAATTCGCGGCCGAGAAATTTTCTTTTCTTTT 3'], double-stranded
 cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not
 I and cloned into the Not I and Eco RI sites of the modified pT73
 vector. Library went through one round of normalization. Library
 constructed by Bento Soares and M.Fatima Bernaldo.

ORGANISM Homo sapiens
 Eukaryote; Metazoa; Eumetazoa; Bilateria; Coelomata;
 Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
 Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria;
 Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 516)
 Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
 Holman,M., Hulman,M., Kucaba,T., Le,M., Lennon,G., Merra,M.,
 Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
 Trevasakis,E., Waterston,R., Williamson,A., Wohlmann,P., and
 Wilson,R.
 The WashU-Merck EST Project
 Unpublished (1995)

JOURNAL MEDLINE
 COMMENT

NID	g1953455
KEYWORDS	FCT

ACCESSION AA300891

KEYWORDS EST.

SOURCE human.
ORGANISM Homo sapiens
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 303)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fullner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodex,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Uterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Melsner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)
MEDLINE 96026280
COMMENT Other-ESTs: THC167177
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tadb/hgi/hgi.html>)
Seq primer: M13 Reverse.
Location/Qualifiers
FEATURES
source
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/note="Organ: testis; Vector: pbluescript SK-; Site_1: EcoRI; Site_2: XhoI"
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Best Local Similarity 75.4%; Pred. No. 2,92e-284; Indels 0; Gaps 0;
Matches 221; Conservative 0; Mismatches 72;
Db 7 ATGAGGGTCCCGCTCAGCTCCTGGGCTCCTGCTACTGCTCGAGTGCAGATGT 66
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RESULT 9
LOCUS AA361497 357 bp mRNA EST 21-APR-1997
DEFINITION EST71040 T-cell lymphoma Homo sapiens cDNA 5' end similar to immunoglobulin kappa light chain, V region, mRNA sequence.
ACCESSION AA361497
NID 92014052
KEYWORDS EST
SOURCE human.
ORGANISM Homo sapiens
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 357)
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fullner,R.A., Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitchhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodex,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Uterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Melsner,P.S., Olsen,H., Raymond,L., Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.
TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
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MEDLINE 96026280
COMMENT Other-ESTs: THC167177
Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tadb/hgi/hgi.html>)
Seq primer: M13 Reverse.
Location/Qualifiers
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Best Local Similarity 74.3%; Pred. No. 6.04e-282; Indels 2; Gaps 2;
Matches 246; Conservative 0; Mismatches 83;
Db 6 ATGAGGTCCCGCTCAGCTCCTGGGCTCCTGCTACTGCTCGAGTGCAGATGT 65
Y 1 ATGGGGGCCCTGCTCAGATCTTGGGTTCTTGTGCTCTGTTCCAGTACAGATGT 60
Db 66 GACATCCAGATGACCCAGTTCCTCCTGTTGATGATCTNAGAGACAGATCAC 125

Qy	61	GACATCCCGAGTACCCAGTCCCTCCCTTATCTCCCTCTCTGGACAAAGAGTCAGT	120
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SEQUENCE	NONION	EST11648	Testis tumor	Homo sapiens	CDNA 5' end similar to	
ACCESSION		AA300788	immunoglobulin kappa light chain, V region,	mrna	sequence.	
NID		q1953120				
KEYWORDS		EST.				
SOURCE		human.				
ORGANISM		Homo sapiens				

REFERENCE

AUTHORS

LE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
JOURNAL Nature 377 (6547 Suppl.), 3-174 (1995)
MEDLINE 96026280
COMMENT Other ESRs: THC167177

FEATURES

Source

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QY 1 ATGGGGGCCCCCTGCTCAGATTCTTGGGTCTTGTGCTCTTGTTCAGGTACCAGATGT 60

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[illegible]

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241 AGGTTCAAGTGGCAGTAGGTTCTGGGTCAAGATTATTTCTCTCACCATCAGCAGCT 293

LOCUS	AA300491	282 bp	mRNA	EST	18-APR-1997
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immunoglobulin kappa light chain, V region, mRNA sequence.

NID
g1952905
KEVIN@BNC
ECM

SOURCE ORGANISM	human.	Homo sapiens
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100	100	100

Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominid

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based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl.) 3-17A (1995)

MEDLINE 96026280
 COMMENT Other ESTs: THC167177

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Thu Apr 15 18:01:37 1999; Maspar time 7.49 Seconds

Output: 330.677 Million cell updates/sec

Output not generated.

Title: >US-08-836-455-4

Description: (1-153) from US08836455.pep

Perfect Score: 1109

Sequence: 1 MECSWVFLFLSLITGVHSQ.....TVSSAKTPPPYPLVPGSL 153

Scoring table:

PAM 150
Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 08
Listing first 45 summaries

Database:

a-genesec32

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29

Statistics: Mean 30.945; Variance 171.704; scale 0.180

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	1109	100.0	153	25	W27120	Murine monoclonal ant	1.22e-73
2	880	76.6	145	13	R66758	Anti-tobacco mosaic v	6.81e-54
3	820	73.9	159	1	P93079	Heavy chain of monocl	1.29e-51
4	798	72.0	146	3	R13061	Monoclonal antibody O	6.01e-50
5	774	69.8	146	8	R40384	Monoclonal antibody M	3.95e-48
6	768	69.3	146	22	W14940	3F4 (Chimeric) human	1.13e-47
7	768	69.3	146	22	W14938	3F4 (Chimeric) human	1.13e-47
8	768	69.3	146	22	W14941	Murine anti-porcine v	1.13e-47
9	768	69.3	146	29	W41070	3F4 Human IgG4 expres	1.13e-47
10	755	68.1	140	29	W47513	Mouse 2H7 antibody he	1.08e-46
11	755	68.1	140	29	W47513	Mouse 2H7 antibody he	1.08e-46
12	755	68.1	140	29	W47513	Mouse 2H7 antibody he	1.08e-46
13	752	67.8	140	23	W16343	2H7 heavy chain varia	1.83e-46
14	752	67.8	140	1	P94780	2 H7 VH gene.	1.83e-46
15	752	67.8	140	22	W10242	Heavy chain variable	1.83e-46
16	749	67.5	140	2	P70627	2H7 antibody heavy ch	1.83e-46
17	749	67.5	140	2	P70627	Sequence encoded by t	3.08e-46
18	745	67.2	590	28	W31751	H chain subunit of Fa	6.19e-46

19	742	66.9	464	13	R76088	Mab 55.1 heavy chain.	1.04e-45
20	741	66.8	235	7	R41682	Cimeric antibody comp	1.24e-45
21	736	66.4	235	7	R41715	Murine 128.1 VH/human	2.96e-45
22	736	66.4	235	7	R41707	Murine 128.1 VH/human	2.96e-45
23	735	66.3	136	1	P93151	Protein encoded by V	3.53e-45
24	735	66.3	136	10	R59510	Sequence of the heavy	3.53e-45
25	730	65.8	141	5	R09427	ME4 Heavy Chain V Reg	8.42e-45
26	730	65.8	141	20	W06216	Mab ME4 heavy chain v	8.42e-45
27	728	65.6	118	25	W27122	Murine antibody heavy	1.19e-44
28	720	64.9	140	20	W06213	Mab Co-1 heavy chain	4.80e-44
29	719	64.8	144	2	R08346	Heavy chain variable	5.71e-44
30	716	64.6	233	7	R41710	Murine 128.1 VH/human	9.62e-44
31	713	64.3	139	28	W36167	Heavy chain variable	1.62e-43
32	711	64.1	137	12	R62445	81C6 heavy chain vari	2.26e-43
33	711	64.1	139	25	W29750	Anti-HMG Mab CTMO1 h	2.29e-43
34	710	64.0	138	27	W34515	Variable heavy chain	2.73e-43
35	710	64.0	140	5	R09425	Co-1 Heavy Chain V Re	2.73e-43
36	704	63.5	139	7	R33950	CTMO1 VH.	7.74e-43
37	704	63.5	249	15	R77609	Chimeric heavy chain	7.74e-43
38	703	63.4	163	3	R15200	R6-5-D6 anti-ICAM-1 h	9.21e-43
39	703	63.4	163	3	R15060	Murine anti-ICAM mono	9.21e-43
40	701	63.2	137	20	W03724	Anti-human gp39 Mab 3	1.30e-42
41	699	63.0	140	10	R55554	DREG-200 Ab heavy cha	1.85e-42
42	697	62.8	137	2	R12238	Mouse Mab 4D12 H chal	2.61e-42
43	697	62.8	137	2	R12360	Heavy chain variable	2.61e-42
44	686	62.8	140	11	R55215	Murine variable regio	3.11e-42
45	695	62.7	136	20	W06446	Humc3 VH region BR-R	3.70e-42

ALIGNMENTS

RESULT	1	W27120 standard; Protein; 153 AA.
AC	W27120;	
DT	04-JAN-1998 (first entry)	
DE	Murine monoclonal anti-idiotypic antibody 11D10 VH region.	
KW	Monoclonal antibody 11D10; anti-idiotypic antibody; muncin.	
KW	human milk fat globule; HMGF; tumour; breast cancer; vaccine.	
OS	Mus musculus.	
FT	Key	Location/Qualifiers
FT	Peptide	1..19
FT	Protein	/label= sig_peptide
FT		20..153
FT		/label= Mat_protein
FT		20..49
FT	Region	/label= FRI
FT		/label= "framework region 1"
FT		50..54
FT		/label= CDR1
FT		/label= "complementarily determining region 1"
FT	Region	/label= FR2
FT		55..68
FT		/label= FR2
FT	Region	/label= "framework region 2"
FT		69..85
FT		/label= CDR2
FT		/label= "complementarily determining region 2"
FT	Region	86..117
FT		/label= FR3
FT		/label= "framework region 3"
FT		118..126
FT		/label= CDR3
FT		/label= "complementarily determining region 3"
FT	Region	127..137
FT		/label= FRI
FT		/label= "framework region 4"
FT	Region	138..153
FT		/label= Constant
PN	W09122699-A2.	
PD	26-JUN-1997.	
PR	19-DEC-1996; U20757.	
PR	13-DEC-1996; US-575762.	
PR	20-DEC-1995; US-575762.	
PR	26-JAN-1996; US-591965.	

PA	(KENT) UNIV KENTUCKY.
PI	Chatterjee M, Chatterjee SK, Foon KA;
PR	WPI; 97-341690/31.
DR	N-PDSB; T85150.
PT	Monoclonal anti-idiotypic antibody 11D10 - elicits immune response
PN	against human milk fat globule disease associated tumours,
PS	especially breast cancer
CS	Claim 10; Page 94-95; 130pp; English.
CC	This polypeptide sequence comprises the heavy chain variable region
CC	(VH) of monoclonal anti-idiotypic antibody 11D10 produced by
CC	hybridoma cell line ATCC 12020. 11D10 was obtained by immunising
CC	nave mice with MC-10 anti-HMFG antibody to obtain an anti-idiotypic
CC	response. It elicits an immune response against a specific epitope
CC	of a high mol.wt. mucin of human milk fat globule (HMFG). It
CC	induces an immunological response to HMFG in mice, rabbits, monkeys
CC	and patients with advanced HMFG-associated tumours. Pharmaceutical
CC	compositions and vaccines comprising 11D10, 11D10 polypeptides
CC	and/or 11D10 polynucleotides (see also T85149-50) are claimed.
CC	Also claimed are diagnostic kits and methods of using 11D10, 11D10
CC	polypeptides and/or 11D10 polynucleotides, including methods of
CC	treating HMFG-associated tumours. 11D10 is also used in a claimed
CC	method of palliating HMFG-associated disease and in claimed kits to
CC	detect or quantify anti-HMFG antibody.
SQ	Sequence 153 AA:
Query Match	100.0%; Score 1109; DB 25; Length 153;
Best Local Similarity	100.0%; Pred. No. 1,22e-73;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Dd	1 mecsvrfifllsitgtvhsgeylqgsgaeilvrsgasvkmckasgytltsymhwkqlp 60
Oy	1 MECSWFELFLSLITGGVSAOAYLLOOSGAEILVRASAVMKSCAKAGYTLLTSNMHWKQTP 60
Dd	61 ggglewignipdgndtyknngfkfkaaltdstssraymgissltedsayfcargnw 120
Oy	61 GGGLWMINIRPGNDIYYNOKFKGKASLDADTSSSTRAYMOISLTSEDSAYFCARGNW 120
Dd	121 egaldywgqgsvevsasakttpppyplvpagl 153
Oy	121 EGALDYWGQGSVTYSSAKTTPPPYPLVPSTL 153
RESULT 2	
ID	R66758 standard; Protein; 465 AA.
AC	R66758;
DT	01-SEP-1995 (first entry)
DE	Anti-tobacco mosaic virus monoclonal Ab heavy chain.
KK	Tobacco mosaic virus; TMV; monoclonal antibody.
KK	heavy chain; virus-resistant plants; biofarming.
OS	Synthetic.
FH	Key
FT	peptide
FT	1..19 Location/Qualifiers
FT	/label= leader
FT	20..465
FT	/label= mat.peptide
FT	20..128
FT	/note= "variable heavy domain"
FT	129..141
FT	/note= "J heavy 4 domain"
FT	142..465
FT	/note= "constant heavy domain"
PN	J06319396-A.
PD	22-NOV-1994.
PF	07-MAY-1993; JP-131208.
PR	07-MAY-1993; JP-131208.
PA	(NTSB) JAPAN TOBACCO INC.
PA	(KURS) KURARAY CO LTD.
DR	WPI; 95-040220/06.
DR	N-PDSB; 079930.
PT	Transformed plant producing animal-derived anti-virus antibody -
PT	esp. tobacco plants producing anti-tobacco mosaic virus
PT	monoclonal antibody
ES	Example 2; Pages 14-15; 26pp; Japanese.

```
CC Q79929 and Q79930 encode R66757 and R66758, the light and heavy chains of an animal derived anti-tobacco mosaic virus (TMV) monoclonal antibody. The cDNAs were incorporated into a Ti plasmid vector, which was incorporated into A. tumefaciens. The resultant plant expression vector was used to transform tobacco plants, making them TMV resistant, the plants could also be bioformed for the prodn. of anti-virus antibodies.
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CC CC also be bioformed for the prodn. of anti-virus antibodies.  
SQ Sequence 465 AA;  
  
Query Match 76.6%; Score 850; DB 13; Length 465;  
Best Local Similarity 76.3%; Pred. No. 6,81e-34;  
Matches 119; Conservative 19; Mismatches 14; Indels 4; Gaps 3;  
  
Db 1 mecmwiflffitsvsgyvsqvlqgssgaelaipgasvkmsckasgyftaymhwkxqp 60  
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
QY 1 MECSWVFELFLSITTGVSQAIVLDOOSGAELVRSGASVKMSCKKASGTYLTSTNNHWAKTP 60  
1 MECSWVFELFLSITTGVSQAIVLDOOSGAELVRSGASVKMSCKKASGTYLTSTNNHWAKTP 60  
  
Db 61 ggglewiaiyppngdtyrtkfkgakatldeakssstajmqslasadsaavycareg 120  
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
QY 61 GGGLIEWIGNIPNGNDITYNOKFKFGKASLTADTSSSTAYAMQISLTSEDSAVYFCAR--G 118  
GGGLIEWIGNIPNGNDITYNOKFKFGKASLTADTSSSTAYAMQISLTSEDSAVYFCAR--G 118  
  
Db 121 yswdyamdwyvggtstvtsakttppvyplapgs 156  
:|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
QY 119 -NMWG-ALDYGOGISTVYSVSAKTTPPYPLVPGS 152  
-NMWG-ALDYGOGISTVYSVSAKTTPPYPLVPGS 152  
  
RESULT 3  
ID Pj3079 standard; peptide, 159 AA.  
AC Pj3079;  
DT 15-MAR-1990 (first entry)  
DE Heavy chain of monoclonal antibody 6A4.  
KW Monoclonal antibody 6A4; heavy chain; pseudomonas aeruginosa; OMP-1.  
PN EP-338395-A.  
PT 25-OCT-1989.  
PF 12-APR-1989; 106463.  
PR 19-APR-1988; DE-813023.  
PA (BEHM) Behringwerke.  
PI Domdey H, Margel M, von Specht BU;  
WP1: 89-310861/43.  
DR N-PSDB; N91643.  
FT Monoclonal antibody to Pseudomonas aeruginosa - and DNA coding for variable antibody regions.  
PS Claim 1; page 6; 7pp; german.  
CC The peptide is encoded by the heavy chain of monoclonal antibody 6A4.  
CC 6A4 reacts with the OMP-1 protein of all 19 known serotypes of P.aeruginosa. It is used for therapy and diagnosis of infection, and as a carrier for drugs. The antibody is IgG2a subclass.  
SQ Sequence 159 AA;  
  
Query March 73.9%; Score 820; DB 1; Length 159;  
Best Local Similarity 76.3%; Pred. No. 1.29e-51;  
Matches 116; Conservative 17; Mismatches 17; Indels 2; Gaps 1;  
  
Db 1 mernwifflfsvtagvhsqvqlqgssgaelaipgasvkmsckasgyftaymhwkxqp 60  
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
QY 1 MECSWVFELFLSITTGVSQAIVLDOOSGAELVRSGASVKMSCKKASGTYLTSTNNHWAKTP 60  
MECSWVFELFLSITTGVSQAIVLDOOSGAELVRSGASVKMSCKKASGTYLTSTNNHWAKTP 60  
  
Db 61 ggglewiaiyppngdtyrtkfkgakatldeakssstajmqslasadsaavycareg 120  
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
QY 61 GGGLIEWIGNIPNGNDITYNOKFKFGKASLTADTSSSTAYAMQISLTSEDSAVYFCAR-- 118  
GGGLIEWIGNIPNGNDITYNOKFKFGKASLTADTSSSTAYAMQISLTSEDSAVYFCAR-- 118  
  
Db 121 nyegamdywggtstvtsakttppvyplap 152  
:|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||  
QY 119 NMEGALDIWGGGTSTVYSVSAKTTPPYPLVP 150  
NMEGALDIWGGGTSTVYSVSAKTTPPYPLVP 150  
  
RESULT 4  
ID R13061 standard; Protein; 468 AA.  
AC R13061;  
DT 03-OCT-1991 (first entry)  
DE Monoclonal antibody OK3T heavy chain.  
KW OK3T; Light chain; humanised antibodies; CDR-grafting.  
MS Mus musculus.
```

FT	Key	Location/Qualifiers
FT	peptide	1..19
FT		/label= signal peptide
FT	protein	20..468
FT		/label= light chain
PN	WO9109967-A.	
PD	11-JUL-1991.	
PF	21-DEC-1990.	G02017.
PR	21-DEC-1989.	GB-028874.
PR	21-DEC-1990.	WO-G02017.
PA	(CELL-) CELLTTECH LTD.	
PI	Agairi JR, Arhwal DS, Emtage JS;	
DR	WPI; 91-222915/30.	
DR	N-PSDB; Q12637.	
PT	New humanised antibodies comprising CDR grafted antibody - with heavy and light chains, for use in in vivo therapy and diagnosis	
PS	Disclosure; Fig 2b; 91pp; English.	
CC	The OK3T heavy chain sequence was deduced from the cDNA sequence isolated from a library prepared from OK3T producing cells. The library was screened with a probe complementary to a region in the mouse IgG2a constant domain region. The OK3T sequence was used in CDR-grafting experiments to prepare humanised antibodies.	
50	Sequence	468 AA;

Query Match	72.0%;	Score 798;	DB 3;	Length 468;
Best Local Similarity	74.3%;	Pred. No. 6.01e-50;		
Matches	113;	Conservative	16;	Mismatches 20;
			Indels	3;
			Gaps	2;

[illegible]

ID	RESULT	5
AC	RA0384 standard; protein; 469 AA.	
DT	RA0384;	
DE	08-FEB-1994 (first entry)	
DE	Monoclonal antibody M(alpha)-2-3 Heavy-chain.	
KW	anti-snake small neurotoxin antibody; heavy chain; IgG3;	
KT	immunoglobulin; bispecific bivalent antibody; cell-targeting;	
KT	cytotoxic agent.	
FT	Key	
FT	peptide	Location/Qualifiers
FT		1..19
FT	region	/label= signal_peptide
FT		20..139
FT	region	/label= variable
FT		140..236
FT	region	/label= constant
FT		237..252
FT	region	/label= joining
FT		253..362
FT	region	/label= constant
FT		363..469
FT	region	/label= constant
PN	EP-556111-A.	
PD	18-AUG-1993.	
PF	09-FEB-1993; 400323.	
PR	11-FEB-1992; FR-001505.	
PA	(BOUL/) BOULAIN J.	
PA	(COMS) COMMISSARIAT ENERGIE ATOMIQUE.	
PI	Boulain J, Ducancel F, Gallet D, Menez A;	
DR	WPI: 93-260351/33.	
DR	N-PSDB: 048037.	
PT	New immunoglobulin hybrid proteins - with immunoglobulin fragments linked to dimeric protein, for diagnostic or	

PT therapeutic use
PS Example 1; Fig 3A; 37pp; French.
CC A fragment of the heavy chain (VH + CH1) from the anti-snake small
CC neurotoxin monoclonal antibody M(alpha)2-3 was PCR-amplified from
CC hydriomax-derived cDNA using primers Q48039 and Q48040. A light
CC chain fragment (VL + CL) was amplified from the same source using
CC primers Q48041 and Q48042. The two amplified fragments were
CC inserted into the same vector; the H-chain fragment was inserted
CC (in-frame) between codons 6-7 of the phoA coding sequence and the
CC L-chain fragment was inserted into a cassette which contained a
CC phoA 5-D sequence, a signal peptide and the first 6 codons of phoA.
CC The cassette was positioned between the termination codon and
CC the transcription termination sequence of phoA. The fusion
CC construct is expected to encode a hybrid protein comprising two
CC identical Ab-derived units. The invention also covers hybrid
CC proteins containing two different Ab-derived units (i.e. to produce
CC bispecific antibodies). When a toxic protein is used in place of
CC phoA, the hybrid molecules can be used as cell-targeting
CC therapeutic agents.
SQ Sequence 469 AA;

Query Match	69.8%;	Score 774;	DB 8;	Length 469;
Best Local Similarity	72.5%;	Pred. No. 3,956-48;		
Matches	108;	Conservative	22;	Mismatches 17; Indels 2; Gaps 1;

Db	4	swifellflstgagahbcqlqdgspvelvbkqasvskscasgytftdyuanvkkqkpgg	63
Oy	4	SMVEFLFLSTITGVHSDAYLDQSCAEVLVRSOASVKMSCKASGYTLTGYNNHNVKKQRLPGG	63
Db	64	lkxvllvlpasgdkklynefnfkqkaltlvdfssstaxmqlsltsedgafvccaragata	123
Oy	64	LEWIGNIFPGKGRDLYVKNQFKRGSALRADSSSRVAYQISLTSDEDSAVIFCAR--GNME	121
Db	124	tlilgyvggtlcltvsaktappsvyrlap	152
Oy	122	GALLIWDGGSIVLVSAAKTYPPPYPLVP	150

RESULT 6
ID W19940 standard; Protein: 463 AA.
AC W19940;
DT 16-JUN-1997 (first entry)
DE 3F4 (Chimeric) human G2/G4 chimeric antibody.
KW xenotransplantation; graft rejection; cell interaction; pig;
KW vascular cell adhesion molecule; VCAM; monoclonal antibody;
KW chimeric antibody; diagnosis.
OS Chimeric Homo sapiens;
OS Chimeric Mus sp.
PN W09711971-AL.
PD 03-APR-1997.
PE 27-SEP-1996; U15575.
PR 28-SEP-1995; US-004489.
PR 26-SEP-1996; US-004489.
PA (ALEX-) ALEXION PHARM INC.
PI Evans MJ, Matlis LA, Mueller EE, Mueller JP, Rollins S;
PI Roeder RP;
DR WPI: 97-212855/19.
DR N-PSDB; T62937.
PT Antibodies binding to porcine but not human cell interaction
PT proteins - useful to treat and assay for rejection of xenografted
PT porcine organs, tissues or cells.
PS Disclosure; Page 58-61; 105pp. English.
CC A chimeric antibody (W19940) comprises the C1 and hinge regions of
CC human IgG2 and the C2 and C3 regions of human IgG4 (G2/G4 MAb) and
CC a murine anti-porcine soluble vascular cell adhesion molecule (VCAM)
CC monoclonal antibody (MAb) 3F4 heavy chain variable region sequence
CC (see also W14938). The chimeric antibody is specific for porcine
CC VCAM. It is useful for diagnosing human rejection of porcine
CC xenotransplants and for improving xenotransplantation of porcine
CC cells, tissues and organs into human recipients.
SQ Sequence 463 AA;

Query Match 69.38; Score 768; DB 22; Length 463;


```

FT      region      118..130
FT      /label= CDR3
FT      /note= "Complementarity determining region 3"
FT      region      131..140
FT      /label= FR4
FT      /note= "framework region 4"
PN      US5618920-A.
PD      08-APR-1997.
PF      01-NOV-1985. 793980.
PR      01-NOV-1985. US-793980.
PR      27-OCT-1986. WO-002269.
PR      24-JUL-1987. US-077528.
PR      11-JAN-1988. US-142039.
PR      29-MAR-1990. US-501092.
PR      17-APR-1992. US-870404.
PR      29-APR-1994. US-235225.
PA      (XOMA ) XOMA CORP.
PI      Better 'M. Horwitz AH, Lei S, Liu AY, Robinson RR;
PI      Wall R, Wilcox GL;
PI      WPI: 97-225473/20.
PI      N-PSDB: T70868.
FT      Secreted immunoglobulin heavy and light chain fragments - capable
FT      of assembling into chimeric antibodies, useful for e.g. passive
FT      immunisation, diagnosis, etc
PS      Example 4; Fig 21; 96pp; English.
CC      A polypeptide (W15343) comprises the heavy chain variable region of
CC      mouse monoclonal antibody 2H7, which recognises human B-cell surface
CC      antigen Bp35. It is encoded by a cDNA clone (T70868) obt. from a
CC      2H7 cDNA library by PCR amplification. The 2H7 light chain variable
CC      sequence (W16344) is also provided. A novel human-mouse chimeric
CC      antibody with specificity for the human B-cell antigen has been
CC      constructed.
CC      Sequence 140 AA:

```

Query Match	67.8%	Score 752;	DB 23;	Length 140;
Best Local Similarity	79.3%	Pred. No. 1,83e-46;		
Matches 111;	Conservative 11;	Mismatches 14;	Indels 4;	Gaps 2;
Db	1	mgfsrifi1flsvctgvhsqaylqgsqgaelyrpsavkmsckasgyctfsynmhvbkqtp	60	
Qy	1	MECSWVFLFLSITTTGVHSQAYLQDSGHELYRSGASVSKASGCTLTSTNMHWKQTP	60	
Db	61	rfglewlgailypgnqdsynqkfkykatltvdkssstlaqmglsitdsedavfcarvvy	120	
Qy	61	GQGLEWIGINIPFGNGDFTYNNQKFKGKASLFLADTSSSTRAVMQISSLTSEDSDAVFYCARNG-N	119	
Db	121	ysnsywyfdivvgvtgtttvts	140	
Qy	120	MEGA--LDYWGQGTSTVTVS	136	
RESULT	14			
ID	P94780	standard; protein; 140 AA.		
AC	P94780;			
DT	06-JUL-1990	(first entry)		
DE	2 H7 VH gene.			
KW	Antibodies; passive immunisation; pH3-12a; ss.			
OS	Synthetic.			
FH	Key	Location/Qualifiers		
FT	peptide	1..19		
FT	domain	/label=Leader peptide.		
FT	domain	20..49		
FT	domain	/label=FR1.		
FT	domain	50..54		
FT	domain	/label=CDR1		
FT	domain	55..68		
FT	domain	/label=FR2		
FT	domain	69..85		
FT	domain	/label=CDR2.		
FT	domain	86..117		
FT	domain	/label=FR3.		
FT	domain	118..130		
FT	domain	/label=CDR3.		

FT	domain	131..140
FT		/label=FR4.
FT	domain	108..123
FT		/label=JK2
PN	WO8900939-A.	
PD	9-FEB-1989.	
PE	25-JUL-1988:	02514.
PR	24-JUL-1987:	US-077528.
PA	(TNGE-) Int Genetic Eng. Inc.	
PI	Robinson RR, Liu AF, Horwitz AH, Wall R, Better M;	
DR	WPI: 89-06114/08.	
DR	N-PSDB: N91146.	
PT	Polynucleotide(s) encoding Immunoglobulin molecules -	
PT	used for efficient prodn. of chimeric human or non-human or	
PT	class switched antibodies.	
PS	Disclosure: 7pp; English.	
CC	Sequence carries the variable region of the chimeric immunoglobulin	
CC	sequence. The antibodies are useful in passive immunisation avoiding	
CC	negative immune reactions. They are also useful in assaying and in vitro	
Q	Sequence	140 AA;

Query Match	Best Local Similarity	Score 752;	DB 1;	Length 140;
Matches 111;	Conservative 11;	Mismatches 14;	Indels 4;	Gaps 2;
Db 1	mgfsrffllsvtqgbsaylqsgsaeilyrpsagvksckasgyftsynmhvyrqtp 60			
Qy 1	MECSWVFLFLSLITTYGHSQATYLOQSSAEILYRSGASVYKMSCKRSGITLITSYNNHMKQTP 60			
Db 61	rtglwigaitypngdtsynqkifgkactllvdkssstamqslslseadaavyfcarvvy 120			
Qy 61	GQGLEWIGNIRPGNGDITYYNGKFRGKASLADPTSSSRATYMQISLTSSEDAVYFCARG-N 119			
Db 121	ysnsywyfdwvgtgtttvts 140			
Qy 120	MEGA---LDYWGQGTSTVTS 136			
RESULT 15				
ID W10242	standard; Protein; 140 AA.			
AC W10242;				
DT 06-AUG-1997	(first entry)			
DE	Heavy chain variable sequence of 2H7.			
KE	Peptide lyase; signal sequence; Gram-negative bacterium; immunoglobulin;			
KM	protein production; human; constant region; passive immunisation; toxin;			
KW	serum sickness; anaphylaxis; sweetener; thauimatin; cytoplasm; periplasm;			
KV	antibody; Ig; heavy-chain; hepatitis; mouse; lung carcinoma; cancer;			
KW	myeloma cell.			
OS	Mus musculus.			
FH	Key	Location/Qualifiers		
FT	peptide	1..19		
FT		/note="leader peptide"		
FT	region	20..49		
FT		/note="framework region 1"		
FT	region	50..54		
FT		/note="complementarity determining region 1"		
FT	region	55..68		
FT		/note="framework region 2"		
FT	region	69..85		
FT		/note="complementarity determining region 2"		
FT	region	86..117		
FT		/note="framework region 3"		
FT	region	118..130		
FT		/note="complementarity determining region 3"		
FT	region	131..140		
FT		/note="framework region 4"		
PN	US5576195-A.			
PD	19-NOV-1996.			
PF	01-NOV-1985.	793980.		
PR	01-NOV-1985.	US-793980.		
PR	27-OCT-1986.	WO-002269.		
RR	24-JUL-1987.	US-077528.		

MUSE RELEASE

(TM)

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Msearch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Apr 15 17:59:34 1999; MasPar time 6.06 Seconds
Output not generated. 677.440 Million cell updates/sec

Title: >US-08-836-455-4
Description: (1-153) from US08836455.pep
Perfect Score: 1109
Sequence: 1 MECRWVFLFLSTTGVHSQ.....TVSSAKTTPPPVPLVPGSL 153

Scoring table: PAM 150
Gap 11

Searched: 74019 seqs, 26840295 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot35
1:swissprot

Statistics: Mean 42.568; Variance 72.286; scale 0.589

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Length	ID	Description	Pred. No.
1	709	63.9	140	1	HV02_MOUSE IG HEAVY CHAIN PRECURS	5.71e-138
2	655	59.1	139	1	HV07_MOUSE IG HEAVY CHAIN PRECURS	5.1e-125
3	645	58.2	117	1	HV52_MOUSE IG HEAVY CHAIN PRECURS	1.37e-122
4	636	57.3	117	1	HV14_MOUSE IG HEAVY CHAIN PRECURS	1.96e-120
5	635	57.3	137	1	HV11_MOUSE IG HEAVY CHAIN PRECURS	3.41e-120
6	634	57.2	117	1	HV05_MOUSE IG HEAVY CHAIN PRECURS	5.91e-120
7	616	55.5	117	1	HV06_MOUSE IG HEAVY CHAIN PRECURS	1.19e-115
8	610	55.0	120	1	HV03_MOUSE IG HEAVY CHAIN PRECURS	3.22e-114
9	608	54.8	117	1	HV04_MOUSE IG HEAVY CHAIN PRECURS	9.66e-114
10	607	54.7	138	1	HV48_MOUSE IG HEAVY CHAIN PRECURS	1.67e-113
11	593	53.5	117	1	HV09_MOUSE IG HEAVY CHAIN PRECURS	3.64e-110
12	588	53.0	117	1	HV49_MOUSE IG HEAVY CHAIN PRECURS	5.64e-109
13	588	53.0	117	1	HV12_MOUSE IG HEAVY CHAIN PRECURS	5.64e-109
14	585	52.8	136	1	HV15_MOUSE IG HEAVY CHAIN PRECURS	2.92e-108
15	584	52.7	117	1	HV51_MOUSE IG HEAVY CHAIN PRECURS	5.05e-108
16	578	52.1	118	1	HV51_MOUSE IG HEAVY CHAIN PRECURS	1.35e-106
17	569	51.3	117	1	HV10_MOUSE IG HEAVY CHAIN PRECURS	1.85e-104
18	560	50.5	120	1	HV50_MOUSE IG HEAVY CHAIN PRECURS	2.53e-102
19	550	49.6	121	1	HV01_MOUSE IG HEAVY CHAIN PRECURS	5.94e-100
20	544	49.1	117	1	HV1G_HUMAN IG HEAVY CHAIN PRECURS	1.56e-98
21	539	48.6	117	1	HV1B_HUMAN IG HEAVY CHAIN PRECURS	2.38e-97
22	476	42.9	136	1	HV16_MOUSE IG HEAVY CHAIN PRECURS	1.56e-82
23	464	41.8	114	1	HV00_MOUSE IG HEAVY CHAIN PRECURS	9.94e-80

24	461	41.6	143	1	HV1C_HUMAN IG HEAVY CHAIN PRECURS	4.98e-79
25	442	39.9	117	1	HV3C_HUMAN IG HEAVY CHAIN PRECURS	1.31e-74
26	439	39.6	142	1	HV01_RAT IG HEAVY CHAIN PRECURS	6.52e-74
27	436	39.3	117	1	HV41_MOUSE IG HEAVY CHAIN PRECURS	3.24e-73
28	431	38.9	116	1	HV05_CARAU IG HEAVY CHAIN PRECURS	4.67e-72
29	431	38.9	119	1	HV3L_HUMAN IG HEAVY CHAIN PRECURS	4.67e-72
30	428	38.6	121	1	HV33_HUMAN IG HEAVY CHAIN PRECURS	2.31e-71
31	428	38.6	135	1	HV02_XENLA IG HEAVY CHAIN PRECURS	2.31e-71
32	424	38.2	116	1	HV3T_HUMAN IG HEAVY CHAIN PRECURS	1.94e-70
33	422	38.1	122	1	HV3G_HUMAN IG HEAVY CHAIN PRECURS	5.64e-70
34	419	37.8	119	1	HV40_MOUSE IG HEAVY CHAIN PRECURS	2.78e-69
35	419	37.8	122	1	HV3A_HUMAN IG HEAVY CHAIN PRECURS	2.78e-69
36	417	37.6	117	1	HV42_MOUSE IG HEAVY CHAIN PRECURS	8.06e-69
37	416	37.5	119	1	HV37_MOUSE IG HEAVY CHAIN PRECURS	1.37e-68
38	415	37.4	114	1	HV3B_HUMAN IG HEAVY CHAIN PRECURS	2.33e-68
39	413	37.2	117	1	HV55_MOUSE IG HEAVY CHAIN PRECURS	6.74e-68
40	411	37.1	117	1	HV03_CARAU IG HEAVY CHAIN PRECURS	1.95e-67
41	410	37.0	122	1	HV3H_HUMAN IG HEAVY CHAIN PRECURS	3.31e-67
42	409	36.9	119	1	HV38_MOUSE IG HEAVY CHAIN PRECURS	5.63e-67
43	404	36.4	115	1	HV3F_HUMAN IG HEAVY CHAIN PRECURS	7.96e-66
44	402	36.2	117	1	HV02_CANFA IG HEAVY CHAIN PRECURS	2.30e-65
45	402	36.2	117	1	HV54_MOUSE IG HEAVY CHAIN PRECURS	2.30e-65

ALIGNMENTS

RESULT	ID	Sequence	Standard	PRT	Length
1	HV02_MOUSE	1	STANDARD	PRT	140 AA.
AC	P01746	21-JUL-1986 (REL. 01, CREATED)			
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)				
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)				
DE	IG HEAVY CHAIN PRECURSOR V REGION (9367).				
OS	MUS MUSCULUS (MOUSE).				
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	EUTHERIA; RODENTIA.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-A/J;				
RX	MEDLINE; 82152818.				
RA	SIMS J., RABBITTS T.H., ESTESS P., SLAUGHTER C., TUCKER P.W.,				
RL	CAPRA J.D., SCIENCE 216:309-311(1982).				
DR	EMBL; J00493; G195007.				
DR	PUB; A02028; HYMSG7.				
DR	HSSP; P01789; 6FAB.				
KW	IMMUNOGLOBULIN V REGION; ANTIBIOTIC ANTIBODY; HYBRIDOMA; SIGNAL.				
FT	SIGNAL	1	19		
FT	CHAIN	20	140		
FT	NON_TER	140	140		
SQ	SEQUENCE	140 AA;	15514 MW;	0700D5C8 CRC32;	
Query Match		63.98;	Score 709;	DB 1;	Length 140;
Best Local Similarity		73.08;	Pred. No. 5.71e-138;		
Matches	100;	Conservative	19;	Mismatches	15;
Indels	3;	Gaps	2;		
Db	4	SPFLFLSTAGVHSEVOLOQSGALVIRAGSVKSKASGYFTSYGINWKPQGG	63		
Qy	4	SWFLFLSTTTVHONAVIQSGALVIRAGSVKSKASGYFTSYGINWKPQGG	63		
Db	64	LEWIGYINPGNGYINNEKFKGTLTVDKSSSTAYMOLRSLTSEDSAYVFCARSHYGG	123		
Qy	64	LEWIGYINPGNGYINNEKFKGKASLTADTSSTAYMOLRSLTSEDSAYVFCARSHYGG	122		
Db	124	SYDQDYGCTPLTVSS	140		
Qy	123	SYDQDYGCTPLTVSS	137		
RESULT	2	STANDARD	PRT	139 AA.	
AC	P01751; P01752.				
DT	21-JUL-1986 (REL. 01, CREATED)				

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DT      21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE      01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DR      IG HEAVY CHAIN PRECURSOR V REGION (B1-8 / 186-2).
OS      MUS MUSCULUS (MOUSE).
OC      EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
CC      EUTHERIA; ROSENTIA.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-C57BL/6;
RX      MEDLINE: 81234548.
RA      BOHMELE A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJESKY K.,
RL      BALTIMORE D.
RM      CELL 24:625-637(1981).
CC      -1- THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING
CC      ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL (NPB
CC      ANTIBODIES).
DR      EMBL: J00529; G195115; -.
DR      PIR: A02034; MHMS18.
DR      HSSP: P01810; 1UHL.
DT      IMMUNOGLOBULIN V REGION; SIGNAL.
FT      SIGNAL          1          19
FT      CHAIN           20         139
FT      DOMAIN          20         49
FT      DOMAIN          50         54
FT      DOMAIN          55         68
FT      DOMAIN          69         85
FT      DOMAIN          86        117
FT      DOMAIN          118        124
FT      DOMAIN          125        139
FT      DISULFID        41         115
FT      NON_TER         139        139
SQ      SEQUENCE       139 AA; 15419 MW; DEB2C7DA CRC32;

Query March          59.1%   Score 655; DB 1; Length 139;
Best Local Similarity 69.4%; Pred. No. 5,51e-125;
Matches          93; Conservative 21; Mismatches 18; Indels 2; Gaps 2;

Db      6 IMFLLATATGVSQVVOLODPGAELVPGASVKLSCKASGTFTSYMMHWKOPRGGL 65
      :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY      6 VELFLSTTGVSHQAVYLQDSGAELVSGASVKNKSCAKSGTTLTSTMHHWKKQPPGLE 65
      |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      66 WIGRIDPNISGGTKINEKRKSKATLTVDKPSTSTAYMQLSLEDSDSAVYCARDDYGSSY 125
      |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY      66 WIGIFPEPNSGTLYTNOKRKASLTADTSSTAYMOISLTSEDSAVYFCAR-GNMEGA- 123
      ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      126 FDYMGQGTTLTVSS 139
      :|||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
      124 LDYMGQGTSTVSS 137

RESULT      3
ID ID HV52.MOUSE STANDARD; PRT; 117 AA.
AC P06327;
DT 01-JAN-1988 (REL. 06, CREATED)
DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (VH558 AL/44).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
CC EUTHERIA; ROSENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE: 85099340.
RX YANCORBOULOS G.D., ALT F.W.;
RA CELL 40:271-281(1985).
RL EMBL: M13787; G466291; -.
DR PIR: A02029; HVMSA1.
DR HSSP: P01772; 1FOR..
DT IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL          1          19
FT CHAIN           20         117
FT DOMAIN          20         49
FT DOMAIN          50         54
      IG HEAVY CHAIN V REGION (VH558 AL/44).
      FRAMEWORK 1.
      COMPLEMENTARITY-DETERMINING 1.
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FT	DOMAIN	55	68	FRAMEWORK 2.
FT	DOMAIN	69	85	COMPLEMENTARITY -DETERMINING 2.
FT	DOMAIN	86	117	FRAMEWORK 3.
FT	DISULFID	41	115	BY SIMILARITY.
FT	NON_TER	117	117	
SO	SEQUENCE	117 AA;	12971 MW;	A60F2B13 CRC32;

Query Match		58.2%;	Score 645;	DB 1;	Length 117;
Best Local Similarity		77.0%;	Pred. No. 1.37e-122;		
Matches		87;	Conservative	16;	Mismatches 10; Indels 0; Gaps 0;
Db	5 WIFLFLSLGTAGVHCQVLOOQSGPELVKPGALVYISCKASGYTTSYDINKWKORPGGL 64	1-111 1	1-111 1	1-111 1	1-111 1
Oy	5 WFLFLSLTGTGVSHQALLOQSGAELVRSQASVYKMSCKASGYTLTSYNMHWKOTPGGL 64	1-111 1	1-111 1	1-111 1	1-111 1
Db	65 EMIGIYVPGDSTKYNEKFGKALTLTADKSSSTAYMOLSLTSSNSAVYFCAR 117	1-111 1	1-111 1	1-111 1	1-111 1
Oy	65 EMIGIYVPGDSTKYNEKFGKALTLTADKSSSTAYMOLSLTSSNSAVYFCAR 117	1-111 1	1-111 1	1-111 1	1-111 1

RESULT 4		STANDARD;	PRT;	117 AA.
ID	HV14.MOUSE			
AC	P01758;			
DT	21-JUL-1986 (REL. 01, CREATED)			
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)			
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)			
DE	IG HEAVY CHAIN PRECURSOR V REGION (108A).			
OS	MUS MUSCULUS (MOUSE).			
OC	EUKARIOTA; METAEOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
RN	EUTHERIA; RODENTIA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 81245215.			
RA	GIYOL D., ZAUTT R., EFFRON K., RECAVY G., RAM D., COHEN J.B.;			
RL	NATURE 292:426-430(1981).			
DR	EMBL; J00488; G554028; -.			
DR	PIR; A02041; HVMS8A.			
DR	HSSP; P01789; IIGI.			
KW	IMMUNOGLOBULIN V REGION; SIGNAL.			
FT	SIGNAL	1	19	
FT	CHAIN	20	117	IG HEAVY CHAIN V REGION (10A).
FT	NON_TER	117	117	
SO	SEQUENCE	117 AA;	12972 MW;	941C002E CRC32;

Query Match		57.3%;	Score 636;	DB 1;	Length 117;
Best Local Similarity		75.4%;	Pred. No. 1.96e-120;		
Matches		86;	Conservative	16;	Mismatches 12; Indels 0; Gaps 0;
Db	4 SWIFELSLGTAGVHSEVLOOQSGPELVKPGASVYKISCKASGYFTFDYNNMHWKOSHGRS 63	1-111 1	1-111 1	1-111 1	1-111 1
Oy	4 SWIFELSLTGTGVSHQALLOQSGAELVRSQASVYKMSCKASGYTLTSYNMHWKOTPGGL 63	1-111 1	1-111 1	1-111 1	1-111 1
Db	64 LEWIGIYVINGGTGYNOKFRKATLTVDNSSLTAYMELSLTSSDAVYVFCAR 117	1-111 1	1-111 1	1-111 1	1-111 1
Oy	64 LEWIGIYVINGGTGYNOKFRKATLTVDNSSLTAYMELSLTSSDAVYVFCAR 117	1-111 1	1-111 1	1-111 1	1-111 1

RESULT 5		STANDARD;	PRT;	137 AA.
ID	HV11.MOUSE			
AC	P01755;			
DT	21-JUL-1986 (REL. 01, CREATED)			
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)			
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)			
DE	IG HEAVY CHAIN PRECURSOR V REGION (543).			
OS	MUS MUSCULUS (MOUSE).			
OC	EUKARIOTA; METAEOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; RODENTIA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 81244548.			
RA	BOTHWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJEWSKY K.,			
RA	BALTIMORE D.;			
RL	CELL 24:625-637(1981).			

CC -1- THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA MAKING
 CC ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL (NPB
 CC ANTIBODIES).
 DR EMBL: J00539; G195119; -
 DR PIR: A02038; G2MS43.
 DR HSSP: P01772; 1FGV.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 19
 FT CHAIN 20 137
 FT DOMAIN 20 49
 FT DOMAIN 50 54
 FT DOMAIN 55 68
 FT DOMAIN 69 85
 FT DOMAIN 86 117
 FT DOMAIN 118 122
 FT DOMAIN 123 137
 FT DISULFID 41 115
 FT NON_TER 137 137
 SO SEQUENCE 137 AA; 15200 MW; C37539BD CRC32;
 Query Match 57.3%; Score 635; DB 1; Length 137;
 St Local Similarity 67.7%; Pred. No. 3.41e-120;
 Matches 90; Conservative 23; Mismatches 18; Indels 2; Gaps 2;
 Db 6 IMFLATATGVSHVQVLOQPGAEVPGASVSKSCASGYTFTSYMMHWKORPGGLE 65
 QY 6 VFLLSITGVSHQAVLQOSGAEVRSASVSKSCASGYTFTSYMMHWKOTPGGLE 65
 Db 66 WIGRIHPSDSDTYNNOKFKGKATLTVDKSSSTAYMOLSLTSDSAVYFCAR 117
 QY 66 WIGRIHPSDSDTYNNOKFKGKATLTVDKSSSTAYMOLSLTSDSAVYFCAR 124
 Db 125 DYWGQGTFTVSS 137
 QY 125 DYWGQGTFTVSS 137
 RESULT 6
 ID HV03_MOUSE STANDARD; PRT; 117 AA.
 AC P01749;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN PRECURSOR V REGION (3).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 [1]
 RA SEQUENCE FROM N.A.
 RX STRAIN-C57BL/6;
 RX MEDLINE: 81234548.
 RA BOTHWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJEWSKY K.,
 RA BALTIMORE D.;
 RL CELL 24:625-637(1981).
 CC -1- THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES
 CC THAT COULD ENCODE IN REGIONS OF NPB ANTIBODIES.
 DR EMBL: J00536; G554035; -
 DR PIR: A02031; HYMS3.
 DR HSSP: P01810; 1JHL.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 19
 FT CHAIN 20 117
 FT DOMAIN 20 49
 FT DOMAIN 50 54
 FT DOMAIN 55 68
 FT DOMAIN 69 85
 FT DOMAIN 86 117
 FT DISULFID 41 115
 FT NON_TER 117 117
 SO SEQUENCE 117 AA; 13016 MW; 0F12FC8B CRC32;
 Query Match 57.2%; Score 634; DB 1; Length 117;
 Best Local Similarity 75.0%; Pred. No. 5.91e-120;
 RL

Matches 84; Conservative 18; Mismatches 10; Indels 0; Gaps 0;
 Db 6 ILFLVATATGVSHVQVLOQPGAEVPGASVSKSCASGYTFTSYMMHWKORPGGLE 65
 QY 6 VFLLSITGVSHQAVLQOSGAEVRSASVSKSCASGYTFTSYMMHWKOTPGGLE 65
 Db 66 WIGRIHPSDSDTYNNOKFKGKATLTVDKSSSTAYMOLSLTSDSAVYFCAR 117
 QY 66 WIGRIHPSDSDTYNNOKFKGKATLTVDKSSSTAYMOLSLTSDSAVYFCAR 117
 RESULT 7
 ID HV06_MOUSE STANDARD; PRT; 117 AA.
 AC P01750;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN PRECURSOR V REGION (102).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 [1]
 RA SEQUENCE FROM N.A.
 RX STRAIN-C57BL/6;
 RX MEDLINE: 81234548.
 RA BOTHWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJEWSKY K.,
 RA BALTIMORE D.;
 RL CELL 24:625-637(1981).
 CC -1- THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES
 CC THAT COULD ENCODE IN REGIONS OF NPB ANTIBODIES.
 DR PIR: A02032; HYMS02.
 DR HSSP: P01810; 1JHL.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 19
 FT CHAIN 20 117
 FT DOMAIN 20 49
 FT DOMAIN 50 54
 FT DOMAIN 55 68
 FT DOMAIN 69 85
 FT DOMAIN 86 117
 FT DISULFID 41 115
 FT NON_TER 117 117
 SO SEQUENCE 117 AA; 12867 MW; 4BDD1982 CRC32;
 Query Match 55.5%; Score 616; DB 1; Length 117;
 Best Local Similarity 75.7%; Pred. No. 1.19e-115;
 Matches 84; Conservative 17; Mismatches 10; Indels 0; Gaps 0;
 Db 6 ILFLVATATGVSHVQVLOQPGAEVPGASVSKSCASGYTFTSYMMHWKORPGGLE 65
 QY 6 VFLLSITGVSHQAVLQOSGAEVRSASVSKSCASGYTFTSYMMHWKOTPGGLE 65
 Db 66 WIGRIHPSDSDTYNNOKFKGKATLTVDKSSSTAYMOLSLTSDSAVYFCAR 116
 QY 66 WIGRIHPSDSDTYNNOKFKGKATLTVDKSSSTAYMOLSLTSDSAVYFCAR 116
 RESULT 8
 ID HV03_MOUSE STANDARD; PRT; 120 AA.
 AC P01747;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN V REGION (36-65).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 [1]
 RA SEQUENCE FROM N.A.
 RX MEDLINE: 83131846.
 RA SIEKEVITZ M., GEFFER M.L., BRODEUR P., RIBLET R.,
 RA MARSHAK-ROTHSTEIN A.;
 RL EUR. J. IMMUNOL. 12:1023-1032(1982).

-1- FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER DIFFERENTIATED GENES
THAT HYBRIDIZE TO THIS ONE, THE AUTHORS CONCLUDE THAT ALL OF
THESE V REGIONS HAVE REARRANGED TO THE SAME J SEGMENT, JH2.

CC PIR: A02038; HVM57.

DR HSSP: P01789; 6FAB.

KW IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY; HYBRIDOMA.

FT NON_TER 120

SQ SEQUENCE 120 AA; 13307 MW; BBA8CCA1 CRC32;

Query Match 55.0%; Score 610; DB 1; Length 120;
Best Local Similarity 75.4%; Pred. No. 3,22e-114;

Matches 89; Conservative 14; Mismatches 12; Indels 3; Gaps 2;

Db 3 LOOSGAEIVRAGSSVMSCKASGTYFTSYGINVWKORPGGLEIYINGNGTYKNK 62

QY 23 LOOSGAEIVRAGSSVMSCKASGTYFTSYGINVWKORPGGLEIYINGNGTYKNK 82

Db 63 FKGKTLTVDKSSSTAYMOLRLTSDSAVYFCARSVYGGSYFPDYGQGLTVSS 120

QY 83 FKGKSLTADTSSSTAYMOLRLTSDSAVYFCARG-NMEGA--LDYWGQGSTVYSS 137

RESULT 9 STANDARD; PRT; 117 AA.

ID HV04_MOUSE

AC P01748;

DT 21-JUL-1986 (REL. 01, CREATED)

DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)

DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)

DE IG HEAVY CHAIN PRECURSOR V REGION (23).

OS MUS MUSCULUS (MOUSE).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; RODENTIA.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-C57BL/6;

RA MEDLINE: 81234548.

RA BOTHEWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJESKY K.,

RA BALTIMORE D.;

CELL 24:625-637(1981).

CC -1- THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY RELATED GENES

CC THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.

CC PIR: A02030; HVM53.

DR HSSP: P01810; 1JHL.

KW IMMUNOGLOBULIN V REGION; SIGNAL.

FT CHAIN 1

FT SIGNAL 19

FT CHAIN 20

FT SIGNAL 49

FT CHAIN 50

FT SIGNAL 54

FT CHAIN 55

FT SIGNAL 68

FT CHAIN 86

FT SIGNAL 85

FT CHAIN 117

FT SIGNAL 117

FT CHAIN 41

FT SIGNAL 115

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DT 01-AUG-1992 (REL. 23, LAST ANNOTATION UPDATE)

DE IG HEAVY CHAIN PRECURSOR V REGION (TEPC 1017).

OS MUS MUSCULUS (MOUSE).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; RODENTIA.

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE: 84248078.

RA GILLIAM A.C., SHEN A., RICHARDS J.E., BLATTNER F.R., MUSHINSKI J.F.,

RA TUCKER P.W.;

RL PROC. NATL. ACAD. SCI. U.S.A. 81:4164-4168(1984).

DR PIR: A02033; HVM57.

DR HSSP: P01810; 1JHL.

KW IMMUNOGLOBULIN V REGION; SIGNAL.

FT CHAIN 1

FT SIGNAL 20

FT CHAIN 21

FT SIGNAL 138

FT CHAIN 21

FT SIGNAL 49

FT CHAIN 50

FT SIGNAL 54

FT CHAIN 55

FT SIGNAL 68

FT CHAIN 69

FT SIGNAL 85

FT CHAIN 86

FT SIGNAL 117

FT CHAIN 118

FT SIGNAL 127

FT CHAIN 128

FT SIGNAL 138

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FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA: 12890 MW: C97683A2 CRC32:
Query Match 53.5%; Score 593; DB 1; Length 117;
Best Local Similarity 74.1%; Pred. No. 3,64e-110;
Matches 83; Conservative 15; Mismatches 14; Indels 0; Gaps 0;
Db 6 IMFLAATATGVSHSOVQLOQSGAELVKGASVYKLSCKASGYFTSYMMHWKQRPGRGLE 65
VFELFLSTITGVSHSOVQLOQSGAELVKGASVYKLSCKASGYFTSYMMHWKQRPGRGLE 65
Qy 66 WIGRIDPNNGGKRYNEKFKSKATLVDTSSSTAYVQMLHSLTSDSAVYFCAR 117
WIGRIDPNNGGKRYNEKFKSKATLVDTSSSTAYVQMLHSLTSDSAVYFCAR 117
Qy 66 WIGNIFPGNGDIYVYNOKFKGKASLTADTSSSTAYVQMLHSLTSDSAVYFCAR 117
WIGNIFPGNGDIYVYNOKFKGKASLTADTSSSTAYVQMLHSLTSDSAVYFCAR 117
RESULT 12
ID HV49_MOUSE STANDARD: PRT: 117 AA.
AC P06328:
01-JAN-1988 (REL. 06, CREATED)
01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (VH558 B4).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN EUTHERIA; RODENTIA.
RM (1)
RP SEQUENCE FROM N.A.
RX MEDLINE: 85099340.
RA YANCOPOULOS G.D.; ALF F.W.;
RL CELL 40:271-281(1985).
DR EMBL: M13788; G466292; -.
DR PIR: A02035; MMSB4.
DR HSP: P01810; 1JHL.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION (VH558 B4).
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA: 12834 MW: 85692PE5 CRC32:
Query Match 53.0%; Score 588; DB 1; Length 117;
Best Local Similarity 72.3%; Pred. No. 5,64e-109;
Matches 81; Conservative 17; Mismatches 14; Indels 0; Gaps 0;
Db 6 IMFLAATATGVSHSOVQLOQSGAELVKGASVYKLSCKASGYFTSYMMHWKQRPGRGLE 65
VFELFLSTITGVSHSOVQLOQSGAELVKGASVYKLSCKASGYFTSYMMHWKQRPGRGLE 65
Qy 66 WIGNIFPGNGDIYVYNOKFKGKASLTADTSSSTAYVQMLHSLTSDSAVYFCAR 117
WIGNIFPGNGDIYVYNOKFKGKASLTADTSSSTAYVQMLHSLTSDSAVYFCAR 117
RESULT 13
ID HV12_MOUSE STANDARD: PRT: 117 AA.
AC P01756:
21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-NOV-1991 (REL. 20, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V REGION (MOPC 104E).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN EUTHERIA; RODENTIA.
RM (1)
RP SEQUENCE.
RX MEDLINE: 83075344.

RA KERRY M.R., FUHRMAN J.S., SCHILLING J.W., ROGERS J., SIBLEY C.H.,
RL HOOD L.E.;
RL BIOCHEMISTRY 21:5415-5424(1982).
CC -1- THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA PROTEIN HAS
CC ALSO BEEN DETERMINED.
CC -1- THIS PROTEIN BINDS DEXTRAN.
DR PIR: A02039; MMS4E.
DR HSP: P01772; 1EGV.
KW IMMUNOGLOBULIN V REGION; GLYCOPROTEIN.
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55
FT NON_TER 117 117
SQ SEQUENCE 117 AA: 12983 MW: 1F6CC304 CRC32:
Query Match 53.0%; Score 588; DB 1; Length 117;
Best Local Similarity 72.4%; Pred. No. 5,64e-109;
Matches 84; Conservative 14; Mismatches 15; Indels 3; Gaps 2;
Db 4 LQOQSGPELVKPGASVYKMSCKASGYFTDYMKVYKQSHGKSLFEMIGDINPNNGGTSYNOK 63
LQOQSGPELVKPGASVYKMSCKASGYFTDYMKVYKQSHGKSLFEMIGDINPNNGGTSYNOK 63
Qy 23 LQOQSGAELVKGASVYKMSCKASGYFTSYMMHWKQRPGRGLEWIGNIFPGNGDIYVYNOK 82
LQOQSGAELVKGASVYKMSCKASGYFTSYMMHWKQRPGRGLEWIGNIFPGNGDIYVYNOK 82
Db 64 FKGKATLVYDKSSSTAYVQMLHSLTSDSAVYFCARDYDW--YFDVWGAQTYTVSS 117
FKGKATLVYDKSSSTAYVQMLHSLTSDSAVYFCARDYDW--YFDVWGAQTYTVSS 117
Qy 83 FKGKASLTADTSSSTAYVQMLHSLTSDSAVYFCARG--HWEGALDWGQGTSTVSS 137
FKGKASLTADTSSSTAYVQMLHSLTSDSAVYFCARG--HWEGALDWGQGTSTVSS 137
RESULT 14
ID HV15_MOUSE STANDARD: PRT: 136 AA.
AC P01759:
21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-FEB-1991 (REL. 17, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (BC11).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN EUTHERIA; RODENTIA.
RM (1)
RP SEQUENCE FROM N.A.
RX MEDLINE: 82222262.
RA KNAPP M.R.; LIU C.-P.; NEWELL N.; WARD R.B.; TUCKER P.W.; STROBER S.;
RA BLATTNER F.R.;
RL PROC. NATL. ACAD. SCI. U.S.A. 79:2996-3000(1982).
DR EMBL: J00494; G195011; -.
DR PIR: A02042; HVM5B1.
DR HSP: P01789; 1JEL.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 136 IG HEAVY CHAIN V REGION (BC11).
FT NON_TER 136 136
SQ SEQUENCE 136 AA: 15078 MW: E04F1C7F CRC32:
Query Match 52.8%; Score 585; DB 1; Length 136;
Best Local Similarity 61.4%; Pred. No. 2,92e-108;
Matches 81; Conservative 25; Mismatches 25; Indels 1; Gaps 1;
Db 6 IIFFLVATATGVSHSOVQLOQSGPEVYKGVSYKISCKSGGYFTDYAMHWKQSHAKSLE 65
VFELFLSTITGVSHSOVQLOQSGAELVKGASVYKLSCKASGYFTSYMMHWKQRPGRGLE 65
Qy 66 WIGNIFPGNGDIYVYNOKFKGKASLTADTSSSTAYVQMLHSLTSDSAVYFCARGNEGALD 125
WIGNIFPGNGDIYVYNOKFKGKASLTADTSSSTAYVQMLHSLTSDSAVYFCARGNEGALD 125
Db 125 YWGGGTTLVSS 136
YWGGGTTLVSS 136
Qy 126 YWGGGTTVSS 137
YWGGGTTVSS 137
RESULT 15
ID HV13_MOUSE STANDARD: PRT: 117 AA.
AC P01757:
21-JUL-1986 (REL. 01, CREATED)

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DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE 01-NOV-1991 (REL. 20, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V REGION (J558).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUHERIA; RODENTIA.
RN (1)
RP SEQUENCE.
RX MEDLINE: 80078170.
RA SCHILLING J., CLEVINGER B., DAVIE J.M., HOOD L.;
RL NATURE 283:35-40(1980).
CC -I- THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO BIND DEXTRAN
CC DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF WHICH OCCUR IN
CC THE D AND J SEGMENTS.
CC -I- THIS PROTEIN BINDS DEXTRAN.
DR PIR: A26242; MHMS15.
DR HSSP; P01789; 2FGW.
RW IMMUNOGLOBULIN V REGION.
FT DISULFID 22 96 BY SIMILARITY.
FJ NON TER 117 117
S7 SEQUENCE 117 AA; 13024 MW; E7548A05 CRC32;

Query Match 52.7%; Score 584; DB 1; Length 117;
Best Local Similarity 72.4%; Pred. No. 5.05e-108;
Matches 84; Conservative 13; Mismatches 16; Indels 3; Gaps 2;

Db 4 LQOSGPELVKPGASVKMSCKASGYTFETDYMKWKVQSHKSLKLEWIGDINPNNGSTSYNOK 63
OY 23 LQOSGAELVRSASVKMSCKASGYTLTSTNMHWKOTPGGLEWIGNIFPGNGDTTYNOK 82
Db 64 FKGAATLVKSSSTAYMQLNSTSEDSAVYYCARDRYW--YFDVWGAGTYTVSS 117
OY 83 FKGRASLTADTSSSTAYMQLSSTSEDSAVYFCARGN--WEGALDIWGQGTSTVSS 137

Search completed: Thu Apr 15 17:59:47 1999
Job time : 13 secs.

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DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DE 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
CC C49 FAB PRECURSOR (FRAGMENT).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RA ABERGEL C., PADLAN E.A., KASHMIRI S.V.S., MILENIC D., CALVO B.,
RA SCHLOM J.;
RL SUBMITTED (JUN-1992) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: M95575; G193217; -.
DR PFAM: PF00047; 19.
KW SIGNAL.
FT SIGNAL. 1 19 POTENTIAL.
FT CHAIN 20 >134 CC49 FAB.
FT NON_TER 134 134
SQ SEQUENCE 134 AA; 14957 MW; 7EB07046 CRC32;
Query Match 61.0%; Score 676; DB 11; Length 134;
Best Local Similarity 72.3%; Pred. No. 7,49e-129;
Matches 99; Conservative 18; Mismatches 17; Indels 3; Gaps 2;
Db 1 MEMSWFLFELSVTGVSHSOVLOQSDAELVKGASVKISCKASGYTFTDHAHWKOMP 60
OY 1 MEGSWFLFELSVTGVSHSOVLOQSDAELVKGASVKISCKASGYTFTDHAHWKOMP 60
Db 61 EGGLEMIQFSPGNDPDKFNEFKKATLTADKSSSTAYVQLNLSLSEDSAVYFCTRS- 119
OY 61 GGGLEMIQIFPGNDPTYNOKFKKASLTADTSSSTAYVQLNLSLSEDSAVYFCARGNW 120
Db 120 N--MAYWGQSTVTVSS 134
OY 121 EGALDYGQSTVTVSS 137
RESULT 3
ID 061250; PRELIMINARY; PRT; 152 AA.
AC 061250;
DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
DE 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE ANTIGEN, B-CELL RECEPTOR PRECURSOR.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-BALB/C.
RC MEDLINE: 96134009.
RA THIRION S., MOTMANS K., HEYLIEN H., RAUS J., VANDEVYVER C.;
RL IMMUNOGENETICS 43:167-168(1996).
DR EMBL: L43567; G899071; -.
DR PFAM: PF00047; 19.
KW SIGNAL.
FT SIGNAL. 1 19 POTENTIAL.
FT CHAIN 20 152 ANTIGEN, B-CELL RECEPTOR.
FT NON_TER 152 152
SQ SEQUENCE 152 AA; 16517 MW; A83E9253 CRC32;
Query Match 58.4%; Score 648; DB 11; Length 152;
Best Local Similarity 65.7%; Pred. No. 3,41e-122;
Matches 92; Conservative 24; Mismatches 22; Indels 2; Gaps 2;
Db 6 ILFLVATATGVSHSOVLOQSGPELVKPGASVKMSCKASGYTFTSSVMHWKOKAGGLE 65
OY 6 VELFLSTTGVSHSOVLOQSGAELVKGASVKMSCKASGYTFTSSVMHWKOTPGGLE 65
Db 66 WIGYNPNNDYTKYNGKRGKATLTSDKSSSTAYVQLNLSLSEDSAVYFCARGNW 125
OY 66 WIGNTPNGDPTYNOKFKKASLTADTSSSTAYVQLNLSLSEDSAVYFCARGNW-E-GA 123
Db 126 IAYWGQSTVTVSSGESLQF 145
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OY 124 LDYWGQSTVTVSSAKTTPP 143
RESULT 4
ID P97746; PRELIMINARY; PRT; 120 AA.
AC P97746;
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DE 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE MONOCLONAL ANTIBODY 1D11 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE: 96366461.
RA KIMURA N., YOSHIKAWA H., IWAMOTO M., SAKIHAMA T., AKASU F., IZUI S.,
RA UENO A., NAKAJIMA Y., TASAKA K.;
RL HYBRIDOMA 14:523-528(1995).
DR EMBL: S82857; G1835936; -.
DR PFAM: PF00047; 19.
FT NON_TER 1 1
SQ SEQUENCE 120 AA; 13147 MW; 3EA54DB8 CRC32;
Query Match 56.4%; Score 625; DB 11; Length 120;
Best Local Similarity 75.4%; Pred. No. 9,72e-117;
Matches 89; Conservative 15; Mismatches 11; Indels 3; Gaps 1;
Db 3 LQSGVTLARFGASVKMSCKASGYTFTSSVMHWKORPGGLEWIGATYPCNSDTSYNOK 62
OY 23 LQSGAELVRSKGASVKMSCKASGYTFTSSVMHWKOTPGGLEWIGATYPCNSDTSYNOK 82
Db 63 FKRAKLTAVTSASTAYVQLNLSLSEDSAVYCTRDYDGSAGAFDYGQSTVTVSS 120
OY 83 FKRAKSLTADTSSSTAYVQLNLSLSEDSAVYFCARGNWEG--ALDYWGQSTVTVSS 137
RESULT 5
ID 009200; PRELIMINARY; PRT; 118 AA.
AC 009200;
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DE 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE IGG HEAVY CHAIN (FRAGMENT).
OS UNKNOWN.
OC UNCLASSIFIED.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=(NZBXNZ) F1 MOUSE; TISSUE=SPLEEN;
RA PAYELLE-BROCARD B.;
RL SUBMITTED (JAN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: U44925; G1763747; -.
DR PFAM: PF00047; 19.
FT NON_TER 1 1
FT NON_TER 118 118
SQ SEQUENCE 118 AA; 12937 MW; FF570A07 CRC32;
Query Match 55.5%; Score 615; DB 11; Length 118;
Best Local Similarity 75.4%; Pred. No. 2,27e-114;
Matches 89; Conservative 11; Mismatches 18; Indels 0; Gaps 0;
Db 1 QVOLLSEGAELARFGASVKMSCKASGYTFTSSVMHWKORPGGLEWIGATYPCNSDTSY 60
OY 20 QAVLQSGAELVRSKGASVKMSCKASGYTFTSSVMHWKOTPGGLEWIGATYPCNSDTSY 79
Db 61 NOKRKRAKTLTADSSSTAYVQLNLSLSEDSAVYFCARGNGLPFDYWGQSTVTVSS 118
OY 80 NOKRKRAKSLTADTSSSTAYVQLNLSLSEDSAVYFCARGNGLPFDYWGQSTVTVSS 137
RESULT 6
ID 009199; PRELIMINARY; PRT; 118 AA.
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AC 009199;
DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
DT 01-JUL-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE IGM HEAVY CHAIN (FRAGMENT) .
OS UNKNOWN .
OC UNCLASSIFIED.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=(N2BXNZW)F1 MOUSE; TISSUE=SPLEEN;
RL PAYELLE-BROGARD B.;
RA SUBMITTED (JAN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: U44924; GI763745; -.
PRFAM: PF00047; 19.
FT NON_TER 1
FT TER 118
SQ SEQUENCE 118 AA; 13117 MW; 0983B8C5 CRC32;

Query Match
Best Local Similarity 54.6%; Score 605; DB 11; Length 118;
Matches 85; Conservative 17; Mismatches 16; Indels 0; Gaps 0;

Db 1 QVQLQSGAEIVRPGRSYKISKCKASGTYFDYINMWKQRPGGGLEWIGMIFPGSGNTKY 60
| :||:||||:|:||||:||||:||||:|:|:|||||:|:|||||:|:|||||:|:|:|
QY 20 QAVYIQSGAEIVRSGASYKMSCKASGTYLTISYNHMWKQTPGGGLEWIGMIFPGSGITY 79
61 NEKEKGRATLTVDTSSTSTAYVQMLSTLSEDSAVYFCARSYGYGFVAWGGTIVTVA 118
|:||||:||||:||||:||||:||||:||||:|:|:|||||:|:|||||:|:|:|
QY 80 NQKRGKASLTADTSSSTAYVQMLSTLSEDSAVYFCARGMNEGALDVTGCGTSTVTS 137

RESULT 7
ID P97407; PRELIMINARY; PRT; 111 AA.
AC P97407;
DT 01-MAY-1997 (TREMBLREL. 03, CREATED)
DT 01-MAY-1997 (TREMBLREL. 03, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
DE TYPE II COLLAGEN ANTIBODY HEAVY CHAIN VARIABLE REGION (FRAGMENT) .
OS MUS MUSCULUS (MOUSE) .
OC EUKARYOTA; METAQOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/J;
RX MEDLINE: 97257994.
RA ITO H.O., UEDA T., HASHIMOTO Y., IMOTO T., KOGA T.;
RL CELL. MOL. LIFE SCI. 53:51-60(1997) .
RT EMBL: U65538; GI731665; -.
PRFAM: PF00047; 19.
FT NON_TER 1
FT TER 111
SQ SEQUENCE 111 AA; 12444 MW; 6A22312F CRC32;

Query Match
Best Local Similarity 52.6%; Score 583; DB 11; Length 111;
Matches 83; Conservative 11; Mismatches 16; Indels 1; Gaps 1;

Db 1 QVQLQSGAEIARKCTGVKMSCKASGTYLTISYNMWKQRPGGGLEWIGALNPSNGTTEY 60
| :||||:||||:||||:||||:||||:||||:|:|:|||||:|:|||||:|:|:|
QY 20 QAVYIQSGAEIVRSGASYKMSCKASGTYLTISYNHMWKQTPGGGLEWIGMIFPGSGITY 79
61 NQKFKDAIILTADKSSSTAYVQMLSTLSEDSAVYFCAREDEYGHFPIYWGQ 111
|:||||:||||:||||:||||:||||:||||:|:|:|||||:|:|||||:|:|:|
QY 80 NQKRGKASLTADTSSSTAYVQMLSTLSEDSAVYFCARGMNEGA-LDIYWGQ 129

RESULT 8
ID Q35140; PRELIMINARY; PRT; 243 AA.
AC Q35140;
DT 01-JAN-1998 (TREMBLREL. 05, CREATED)
DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE ANTI-CD30 MOAB KI-4 SCEV (FRAGMENT) .

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[illegible]

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C.
RA TAKARA R., MIYAMOTO Y., HONJOH K., SOEDA T., SAKAMOTO J., MIYAMOTO T.,
RL HATANANO S.;
RL SUBMITTED (APR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: D50137; D1024480; -.
DR PRAM: PF00047; 19.
FT NON_TER 1
FT NON_TER 116
FT SEQUENCE 116 AA; 13097 MW; BEF6E1A CRC32;

Query Match
Best Local Similarity 46.3%; Score 513; DB 11; Length 116;
Matches 76; Conservative 16; Mismatches 21; Indels 2; Gaps 1;

Db 4 LQESPELVKPGASVEISIKASGYSTFYIYHMKQSHVKSLEWIGRINPGVISTYNN 63
11:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
23 LQSGAGELVRSGAVKSKCKASGYTTLISYNNHMKQIPGGGLEIGNIFPENGDTIYNOK 82
11:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
64 FKDKASITLVDSKSTAYMEHLSLTSEDSAVYYCAITTVEDYAVDWGQGTIVTSS 116
11:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
83 FKGKASITLADTSSSTAYMOISLTSEDSAVYFCARGNMWEGALDYWGQGTIVTSS 137

RESULT 11
ID 035528 PRELIMINARY; PRT; 120 AA.
AC 035528;
DT 01-JAN-1998 (TREMBL,REL. 05, CREATED)
DT 01-JAN-1998 (TREMBL,REL. 05, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBL,REL. 07, LAST ANNOTATION UPDATE)
DE ANTI-ACID PHOSPHATASE VARIABLE LIGHT CHAIN 11 (FRAGMENT).
MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C.
RA TAKARA R., MIYAMOTO Y., HONJOH K., SOEDA T., SAKAMOTO J., MIYAMOTO T.,
RL HATANANO S.;
RL SUBMITTED (APR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: D50136; D1024479; -.
DR PRAM: PF00047; 19.
FT NON_TER 1
FT NON_TER 120
FT SEQUENCE 120 AA; 13235 MW; 9C34DC15 CRC32;

Query Match
Best Local Similarity 46.3%; Score 514; DB 11; Length 120;
Matches 76; Conservative 19; Mismatches 20; Indels 2; Gaps 2;

Db 4 LKESGPNLVKPGASVKSISCKASGYSTFYIYHMKQSHVKSLEWIGRINPGVISTYNN 63
11:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
23 LQSGAGELVRSGAVKSKCKASGYTTLISYNNHMKQIPGGGLEIGNIFPENGDTIYNOK 82
11:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
64 FNDKASITLVDSKSTAYMEHLSLTSEDSAVYYCAITTVEDYAVDWGQGTIVTSS 120
11:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
83 FKGKASITLADTSSSTAYMOISLTSEDSAVYFCARGNMW-EG-ALDYWGQGTIVTSS 137

RESULT 12
ID P97512 PRELIMINARY; PRT; 249 AA.
AC P97512;
DT 01-MAY-1997 (TREMBL,REL. 03, CREATED)
DT 01-MAY-1997 (TREMBL,REL. 03, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TREMBL,REL. 06, LAST ANNOTATION UPDATE)
DE SINGLE CHAIN FV ANTIBODY (FRAGMENT).
MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RA ARTSARENKO O., WELLER E.W., KUENTZ K., CONRAD U.;

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RN	J. PLANT PHYSIOL.	144:	427-429(1994).
RP	SEQUENCE FROM N.A.		
FX	MEDLINE;	96086099.	
RA	ARTSANKO O., PEISER M., ZUR NIEDEN U., FIEDLER U., WEILER E.W.,		
RL	MUDENT K., CONRAD U.;		
PL	PLANT J. 8;745-750(1995).		
DR	EMBL; 229480; E283450; -		
PFAM;	Pf00047; 19.		
FT	NON_TER	1	
SQ	SEQUENCE	249 AA; 26839 MW; 4289904E CRC32;	
Dd	Query Match	46.3%; Score 514; DB 11; Length 249;	
	Best Local Similarity	62.2%; Pred. No. 1,26e-90;	
	Matches	74; Conservative 18; Mismatches 26; Indels 1; Gaps 1;	
Oy	1 QVALDQSAGAEVLRPGASVKLTCTAAGEFNKDDYIHWWKPREFGLEWIGRIAPASGNVKK 60 : : : : : : : 20 QAVLDQSGAEVLVRGASGYKMCKASGYTLTSYNHWKWQPGLGLEWIGNIFPENGDTYY 79		
Dd	61 VPRPDKATITADSSNTAYLLSLSEDPAAVYCARRDLTYLSLGMOGTIVTWS 119 : : : : : : : : 80 NOKRKGRASILTDISSSTAYMOISLSDESAVFCA-GNWEGALDIWGGISVTYS 137		
RESULT	13 PRELIMINARY; PRT; 98 AA.		
ID	OS5113		
AC	OS5113;		
DT	01-JUN-1998 (TREMBLREL_06, CREATED)		
DT	01-JUN-1998 (TREMBLREL_06, LAST SEQUENCE UPDATE)		
DT	01-JUN-1998 (TREMBLREL_06, LAST ANNOTATION UPDATE)		
DE	A6 ANT1-(4-HYDROXY-3-NITROPHENYL(PHENOLATE FORM) ACETYL NAB V-H REGION (FRAGMENT).		
DS	MUS MUSCULUS (MOUSE).		
OC	EUDAROTA; METAEOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;		
CC	EUTHERIA; RODENTIA.		
RM	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57B2/6;		
FX	MEDLINE; 88198051.		
RA	SOEBANDRIO A., AZUMA T., HAMADA Y., SAKATO N., FUJIO H.;		
RL	J. BIOCHEM. 102;1337-1343(1987).		
DR	EMBL; D00233; D1019624; -		
FT	NON_TER	1	
FT	NON_TER	98	
SQ	SEQUENCE	98 AA; 10865 MW; 4C615AE9 CRC32;	
Dd	Query Match	46.2%; Score 512; DB 11; Length 98;	
	Best Local Similarity	74.2%; Pred. No. 3.70e-90;	
	Matches	72; Conservative 12; Mismatches 13; Indels 0; Gaps 0;	
Oy	1 QVALDQSAGAEVLRPGASVKLTSCNASGYTLFSYWMMWKORPGRGLEWIGRIDPNSSGGTKY 60 : : : : : : : 20 QAVLDQSGAEVLVRGASGYKMCKASGYTLTSYNHWKWQPGLGLEWIGNIFPENGDTYY 79		
Dd	61 NEKRSKATILTVDKPSSSTAYWMOLSLXSDESAUYICA 97 : : : : : : : 80 NOKRKGRASILTDISSSTAYMOISLSDESAUYFCA 116		
RESULT	14 PRELIMINARY; PRT; 125 AA.		
ID	Q09846		
AC	Q09846;		
DT	01-MAY-1997 (TREMBLREL_03, CREATED)		
DT	01-MAY-1997 (TREMBLREL_03, LAST SEQUENCE UPDATE)		
DT	01-JUN-1998 (TREMBLREL_06, LAST ANNOTATION UPDATE)		
DE	PLATELET MEMBRANE GLYCOPROTEIN IB (GPID) SPECIFIC ANTIBODY (FRAGMENT). VI-02.		
CS	HOMO SAPIENTS (HUMAN).		
CC	EUDAROTA; METAEOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;		
CC	EUTHERIA; PRIMATES.		
N	[1]		

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